

# TIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 121495

To: Sarvamangala Devi

Location: REM 3C18 Art Unit: 1645 Thursday, May 13, 2004

Case Serial Number: 10/089787

**Beverly Shears** From: Location: Remsen Bldg.

**RM 1A54** 

571-272-2528 Phone:

beverly.shears@uspto.gov

### Shears, Beverly

From: Sent:

Devi, Sarvamangala

To: Subject: Thursday, May 06, 2004 4:27 PM

Shears, Beverly

10/089,787

### Beverly:

Please perform a sequence and an interference search for SEQ ID NO: 1 and SEQ ID NO: 2 in application SN 10/089,787.

Thanx.

Waland Co

PTO-1590 (9-90)

S. DEVI, Ph.D. AU 1645 Rems - 3C18

1988	STAFF USE ONLY	
Date completed: 05 13-04	Search Site	Vendors
Searcher: Beverly @ 2528	STIC	IG
Terminal time: 20	CM-1	STN
Elapsed time:	Pre-S	Dialog
CPU time:	Type of Search	APS
Total time: 25	N.A. Sequence	Geninfo
Number of Searches:	A.A. Sequence	SDC
Number of Databases:	Structure	DARC/Questel
	Bibliographic	Other CGN

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May 7, 2004, 08:37:38 ; Search time 46 Seconds (without alignments) 2469.273 Million cell updates/sec
                                                                                                                                                                                                       US-10-089-787-2
1837
1 MLLILAEYLQQFYKGFGVFQ......RFWIITVILVLIGLATLKLR 360
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                           Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SPTREMBL\_25:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
7: sp\_page:\*
7: sp\_virus:\*
7: sp\_viru

# SUMMARIES

Description		2 pseudomonas	6 nitrosomona	5 shewanella	6 coxiella bu	4 ralstonia s	7 haemophilus	9 bordetella	0 bordetella	1 bordetella		0 candidatus	1 chlorobium	3 leptospira	2 campylobact	
Bori	Q88n79	Q87wy2	282vs6	Q8e9p5	Q83£26	28xvi4	Q7vp57	7wfr	07vuq0	7w4b	289fu4	27vqj0	28kgd1	Q8f4j3	9pi7	7vgz9
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ID	Q88N79	Q87WY2	Q82VS6	QBE9P5	Q83F26	Q8XVI4	Q7VP57	Q7WFR9	Q7VUQ0	Q7W4B1	Q89FU4	07VQ10	Q8KGD1	Q8F4J3	Q9PI72	6ZDALO
DB	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16
% Query Match Length DB	360	360	361	360	361	389	360	377	377	377	367	365	368	368	353	359
% Query Match	91.9	90.3	71.6	71.1	70.6	0.99	64.6	64.5	64.5	64.3	53.1	45.2	45.1	44.6	42.6	38.4
Score	1689	1658	1314.5	1306	1296.5	1212.5	1186	1184.5	1184.5	1181.5	976	830.5	828	819	782.5	704.5
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# ALIGNMENTS

Database :

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Gaps

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20; Indels

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323; Conservative
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   Matches
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SEQUENCE FKON N.A.

REATY K., Uterback T., Van Aken S., Feldblym T., Gwinn M.,

Buell R., Joardar V., Khouri H., Fedorcova N., Tran B., Russell D.,

Buell R., Joardar V., Wan Aken S., Feldblym T., Gwinn M.,

Dodson R., DeBoy R., Durkin A., Follonay U., Madupu R., Daugherty S.,

Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,

Mitte O., Fraser C., Collmar A.,

"Complete sequence of Pseudomonas syringae.",

"Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, ABOISETI, AAOST860.1;

"Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, Rombitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

"Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

"GO; GO:0006209; P:transferase activity; IEA.

"GO; GO:0006209; P:transferase activity; IEA.

"GO; GO:0006222; P:peptidoglycan biosynthesis; IEA.

InterPro; IPRO03524; PRAcPPept_trans.

"INTERPROPTION (MARAY I: 1.)

"BR PROSITE; PS01348; MRAY_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IEKNSRGLPSRWKYFWQSVFGLAAAVFLYKTAPTSVETTLILPFIKDVTIPLGVGFVVLT 180
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadacee; Pseudomonas.
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                                                                                                                                                   Length 360;
                                                                                                                                           Query Match

91.9%; Score 1689; DB 16; Length
Best Local Similarity 90.3%; Pred. No. 1.5e-114;
Matches 325; Conservative 18; Mismatches 17; Indels
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60 AA; 39484 MW; CF79F93DC0A8CD66 CRC64;
PROSITE; PS01348; MRAY 2; 1.
Transferase; Complete protecme.
SEQUENCE 360 AA; 39307 MW; 91B911C3B411BDE6 CRC64;
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01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase.
MRAY OR PSPTO4411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nitrosomonas europaea.
Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales,
Nitrosomonadaceae, Nitrosomonas.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MraY; phospho-N-acetylmuramoyl-pentapeptide-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Complete proteome.
361 AA; 39264 MW; AC5BF6C9523B2DD9 CRC64;
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17; Mismatches
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Best Local Similarity 69.8
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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MRAY OR NE0988.
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01-JUN-2003 (
01-JUN-2003 (
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                                                                                                                                     61 GPESHFSKRGTPTMGGLLILGAIFLSVLLWGDLGSRYVWYMLFVLGSFGMIGFIDDYRKV 120
                                                                                                                                                                                                                   121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180
                                                                                                                                                                                                                                                   GPOSHLSKKGTPIMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120
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                               1 MLVYLAEYLTRFHTGFNVFSYVTFRAILGILTALMFSLWWGPKLIERLQLMQIGQVVRND
                                                                                                                                                                                                                                                                                                                           181 YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI
                                                                                                                                                                                                                                                                                                                                                           241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKKR
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1 MLLLLAEYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEGUENCE FROM N.A.

SERDIALINE-21608657, PubMed=1704232;

SESHARI-Nine Mile phase I / RSA 493;

SESHAGTI R. Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,

Seshadti K., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,

Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,

DEBON W.T., Deugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,

Rhouri H.M., Lee K.H., Carry H.A., Scanlan D., Heinzen R.A.,

Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;

Trompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;

"Complete genome sequence of the Q-fever pathogen, Coxiella

Durnetii.";

"Complete genome sequence of the Q-fever pathogen, Coxiella

BEL; ARO16960; ARO896891; -.

EMBL; ARO16960; ARO896891; -.

EMBL; ARO16960; ARO896891; -.

EMBL; ARO16960; ARO896891; -.

RO; GO:0010993; F:phosphor-W-acetylmuramoyl-pentapeptide-trans. ..; II.

GO; GO:00109925; P:phosphor-W-acetylmuramoyl-pentapeptide-trans. ..; II.

GO; GO:000925; P:peptidelycan biosynthesis; IEA.

InterPro; IPR00325; P:peptidelycan biosynthesis; IEA.

Frank PR00353; P:phosphor-trans.

Frank PR0053; Glycos trans.

Frank PR0053; Glycos trans.

Frank PR00543; Glycos trans.

Frank PR00543; Glycos trans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Coxiellaceae; Coxiella.
NCBL_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.6%; Score 1296.5; DB 16; Lengt
llarity 67.9%; Pred. No. 3.9e-86;
Conservative 49; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AA; 39537 MW; 4B74157AA0729276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0TN-2003 (TrEMBLrel. 24, Created)
01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase.
MRAY OR CBU0125.
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ses 245; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coxiella burnetii.
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01-JUN-2003 (01-JUN-2003)
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MEDLINE=22297686; PubMed=12368813;

MEDLINE=22297686; PubMed=12368813;

Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

Heidelberg J.F., Paulsen I.T., Nelson M.C.,

Read T.D., Eisen J.A., Scott J., Beanan M., Brinkac L., Daugherty S.,

Meyer T., Todeson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

Madupu R., Peterson J.D., Umyam L.A., White O., Wolf A.M.,

Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

Nameller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;

"Genome sequence of the dissimilatory metal ion-reducing bacterium

IT Shewanella oneidensis.";

Nat. Biotechnol 20:1118-1123(2002).

RMBL; AE015855; AANS7194.1;
                                                                                                                                     121 IQRNSKGLSASSKFFWQSIIALLVAVYLAMTADLPQHTEMIVPFFKEVAIPLGTFLFIVL
                                                                                                                                                                                                                                                   241 AVFCGALTGAGLAFLWFNTYPAEVFMGDVGALALGAALGVITVIVRQEIVLVINGGVFVM
                                                                                                                                                                                                                                                                                                                                                                                                                                   300 ETLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 BALSVMIQVASYKLFGQRVFRMAPLHHYYELKGWKENQVVVFFWIITLILVLIGLSTIKL
                            61 GPQSHLIKAGTPIMGGTLILITAVIVTTLLMADLSNRYIWVVSLTTLGFGAIGWVDDYRKV
                                                                                                     121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIF-FVVL
                                                                                                                                                                                                                                                                                                                           240 IVFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVM
GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
                                                                                                                                                                                                                180 TYPVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGEL
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Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
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GO; GO:0016963; F:phospho-N-acetylmuramoyl-pentapeptide-trans.
GO; GO:0016649; F:transferase activity; IEA.
GO; GO:0016629; P:ipid metabolism; IEA.
GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
InterPro; IPR00315; Glyco trans 4.
InterPro; IPR00315; Glyco trans 4.
InterPro; IPR00354; PNAcPeptt trans.
Ffam; PF00993; Glycos transf 4; I.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase.
MRAY OR S04222.
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PROSITE; PS01348; MRAY 2; 1
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Matches 247; Conservative
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108E9FS
108E9FS
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61 GPQTHLVKAGTPTMGGVLVLIGIAVSTLLMCDWGNRFIWIVLLVTLGYGTIGWVDDYRKY 120
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MLLALAQWLQNDFGFLRVFNYLTFRAVMASLTALVIGLGFGPWVIRRLTELKVGQAVRSY
                                                                            GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
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Pasteurellaceae; Haemophilus.
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Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur Johnson L., Nguyen D., Mang J., Forst C., Hood L.;

The complete genome sequence of Haemophilus ducrey!.";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AB017151; AAP95230.1; --

Transferase; Complete protecome.

Examble AB017151; AAP95230.1; --

Transferase; Complete protecome.
                                                                                                                                                                                                                     121 IEKNSRGLPSRWKYFWQSVFGIGAAVFL-YMTAET-------
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramcyl-pentapeptide-transferase E.
MRAY OR HD0244.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TLSVMIQVASFKLT-GRRVFRMAPIHHFELKGWPDPRVIVRFWIITVLLVLIGLATLKL 359
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                                    GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
                                                                                                                                                                                                                                                                                                                             YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Probable HOSPHO-N-acetylmuramoyl-pentapeptide-transferase
transmembrane protein (EC 2.78.13)
MRAY OR RSC2847 OR RS00258.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria; Betaproteobacteria; Burkholderiales;
NCBL TaxID=305;
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MEDLINE-21681879; Pubmed-11823852;
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Best Local Similarity
Matches 233; Conserva
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SECURINERES O ATCC BAA-588;

X MEDILINE-2827594; PubMed-12910271;

X BEDILINE-2827594; PubMed-12910271;

RA Farris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quall M.A.,

RA Achtuan M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Flewell T., Coble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Flewell T., Coble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Fellwell T., Coble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Babbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Marin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

RI Bordetella parapertussis and Bordetella bronchiseptica.";

NAT. Genet. 35:32-40(2003).
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241 IMCTAIVGAGLGFLWYNTYPAQVFMGDVGSLSLGGALGVIAVLVRQELLLLVMGGVFVVE 300
                                         301 ALSVILQVGSYKLRQKRIFRMAPIHHHFBLKGWPEPRVIVRFWIITLVLVLVLVGLYTLKLR 360
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                         301 TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transfera se (EC 2.7.8.13)
MRAY COR MURX OR BB4201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1184.5; DB 16; Length 377; Pred. No. 5.3e-78; A4; Mismatches 67; Indels 29;
                                                                                                                                                                                                          Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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SEQUENCE 377 AA; 41315 MW; 3440248BAD69BF1C CRC64;
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362 ITMMLVLVGLSTLKLR 377
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62.8%;
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SEQUENCE FROM N.A.

STAIN=CADEMAE 1 / ATCC BAA-589 / NCTC 13251;

STAIN=CADEMAE 1 / ATCC BAA-589 / NCTC 13251;

ATAIN=CADEMAE 1 / ATCC BAA-589 / NCTC 13251;

ATAIN=CADEMAE 1 / Sebaihia M., Preston A., Murphy L.D., Thomson N.,

ATTAIN T. Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Andrean M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Andrean M., Atkin R., Eawer S., Basham D., Bason N., Cherevach I.,

Andrean M., Atkin R., Hamlin M., Cronin A., Davis P., Doggett J.,

Cerlon-Tarriage A., Norberczak H., O'Neil S., Ormond D., Price C.,

Andrean J., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitech B., Rutter S., Sanders M., Saunders D., Seeger K.,

Andrew S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Choparative analysis of the genome sequences of Bordetella pertussis,

Nat. Genet. 35:32-4012033.

BENEL, BEKGHAZO, CARA122911;

RABL, BEKGHAZO, CAMPIELE BROCHER BROCHISEPTICA.";

RABL, BEKGHAZO, CAMPIEL BROCHER BROCHISEPTICA.";

RABL, BEKGHAZO, CAMPIEL BROCHER BROCHISEPTIC CRC64;

SEQUENCE 377 AA, 41315 MW; 3440248BAD69BFIC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 MCGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKVIEKNSRGLPSRWK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFWQSVFGIGAAVFLYMTAETPIET--------TLIVPMLKSVEIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYIPGAAELMVLCAAIGGAGLAFLWFNAYPAQVFWGDVGALALGGALGTIAVIVRQEIVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                      ol-col-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transfera se (EC 2.7.8.13)
MRAY OR MURX OR BP3026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                              Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1184.5; DB
; Pred. No. 5.3e-78;
44; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
  377 AA
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01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                              Bacteria; Proteobacteria; B
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 62.8<sup>3</sup>
Matches 236, Conservative
PRELIMINARY;
                                                                                                                                                                                     Bordetella pertussis
                                                                                                                                                                                                                                                                  NCBI_TaxID=520;
                                             01-0CT-2003 (
01-0CT-2003 (
01-0CT-2003 (
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                                               SEQUENCE
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                                                                                                                       SEQUENCE FROM N.A.

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.TG., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A chtman M., Atkin R., Temple L., James K., Harris B., Cherevach I.,

Cerlingworth T., Collins M., Cranin A., Davis P., Doggett J.,

Chillingworth T., Coble A., Hamlin N., Hauser H., Holroyd S., Uagels K.,

Reltwall T., Goble A., Hamlin N., Hauser H., Holroyd S., Uagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Sanders B., Seeger K.,

Choparative analysis of the genome sequences of Bordetella pertussis,

Nordetella paraportussis and Bordetella bronchiseptica.";

Nordetella paraportussis and Bordetella bronchiseptica.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 MGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKVIEKNSRGLFSRWK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFWQSVFGIGAAVFLYMTAETPIET-------TLIVPMLKSVEIQ 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAIGVFEYITLRAVLACATALLIGLVAGPRVIRRLTEMKIGQAVRAYGPESHLVKTGTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRNDGPQSHLSKKGTPT
                                 (EC 2.7.8.13)
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                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                         Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obium japonicum.
Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                   68; Indels
                                                                                                                                                                                                                                                                                                                                                                  63688099A19A7F28 CRC64;
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01-JTN-2003 (TrEMBLrel. 24, Last sequence update)
01-JTN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MPSSpho-N-actylmuramoyl-pentapeptide-transferas e MRAY OR BLi6605.
Bradyrhizobium japonicum.
01-OCT-2003 (TrEMBLrel. 25, Last sequence update) Phospho-N-acetylmuramoyl-pentapeptide-transfera se maray OR MRX OR BPP3755.
                                                                                                                                                                                                                                                                                                                                                                                          64.3%; Score 1181.5; DB:
62.8%; Pred. No. 8.7e-78;
ive 43; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                    EMBL, BX640434; CAE39038.1; --
Transferase; Complete proteome.
SEQUENCE 377 AA; 41327 MW; (
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|TMMLVLVGLSTLKLR 377
                                                           Bordetella parapertussis.
Bacteria; Proteobacteria; B
Alcaligenaceae; Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                NCBI_TaxID=519;
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Best Local
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Q89FU4
AC Q89FU
DT 01-JU
DT 01-JU
DF Phosp
GN MRAY
OG BRADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFABYLLIPNVPGAGELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOQFYKGFG-----VFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQ-IGQAVRND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 VFCAALVGAGLGFLWFNTYPAQVFWGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 VLCGALLGAGLGFLWFNAPPASIFWGDTGSLALGGWLGAIAVAVKHBIVLAVIGGLFVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 AVSVIVQVVSFKLTGKRIFRMAPIHHHFBGLGWTBPQIVIRFWIISVMLALAGLGTLKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR
                                                                                                                                                                                                                                                                             A language and the complete genomic sequence of nitrogen-fixing symbiotic bacterium T Bradyrhizobium japonicum USDAII0.";

Bradyrhizobium japonicum USDAII0.";

Bradyrhizobium japonicum USDAII0.";

Brabi, APRO05959, BAC51870.1; -.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; F:transferase activity; IEA.

R GO; GO:0016629; P:lipid metabolism; IEA.

R GO; GO:0009522; P:peptidGalycan biosynthesis; IEA.

R InterPro; IPR001524; PNAcPppt trans.

R InterPro; IPR001524; PNAcPppt trans.

R PROSITE; PS01347; MRAY 1: 1.

R PROSITE; PS01347; MRAY 2: 1.

R PROSITE; PS01347; MRAY 2: 1.

M Transferase; Complete proceeme.

SEQUENCE 367 AA; 39570 MW; A176529AED38E3E4 CRC64;
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Candidatus Blochmannia floridanus.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriacese, ant endosymbionts; Candidatus Blochmannia.
                                                                                                                                        MEDLINE-22484998; PubMed=12597275;
Kaneko T. Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                                                                                                    nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22784745; PubMed=12886019;
Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7VQJO;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide transferase (EC 2.7.8.13)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%; Score 976; DB 16; Length 3
52.5%; Pred. No. 6.5e-63;
ive 57; Mismatches 106; Indels
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Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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Matches 189; Conservative
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                                                                                                                                                                                                                                                                                                                                                                           238 ELIVECAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVF 297
                                                                                                                                                                                                                                                                                                                                                                                         241 ELVVVCASIIGAGLGFLWFNSYPSQIFMGDVGSLSLGGVIGLVSILLHQEYLLLIMGGIF 300
                                                                                                                                                                      1 MILLLAEYLQQFYKG--FGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIP-QIGQAV 57
                                                                                                                                                                                      SEQUENCE FROM N.A.

C STRAIN=TLS/ ATCC 46552 / DSM 12025;

MEDLINE=22103685; PubMed=1203901;

A Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., Deboy K.E., Gwinn M.L., Nelson W.C., Haff D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

A Numerhevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Venner J.C., Tettelin H., Bryant D.A., Fraser C.M.;

The complete genome sequence of Chlorobium repidum TLS, a

Proc. Natl. Acad. Sci. U.S. A. 99:9509-9514(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                            VMETLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGL 354
                                                                                                                                                                                                                        RNDGPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDY
Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B., van Ham R.C.H.J., Gross R., Moya A.; "The genome sequence of Blochmannia floridanus: comparative analysis of reduced genomes.";
                                                                                                                                               Gaps
                                                                                                                                              3;
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GO; GO:001803; F:phospho-N-acetylmuramoyl-pentapeptide-trans.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006629; P:lipid metabolism; IEA.
GO; GO:0009252; P:peptidoglyvan biosynthesis; IEA.
InterPro; IPR000715; Glyco_trans_4.
                                                                                                                  Score 830.5; DB 16; Length 365; Pred. No. 2.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
                                                                                                                                              88; Mismatches 111; Indels
                                                       Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).

EMBL. BX248584; CAD33660.1; -.

YEANSferase; Complete proteome.

SEQUENCE. 365 AA; 41504 MW; E7A2EEFC10966B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase.
MRAY OR CT0037.
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                                                                                                                      45.28;
                                                                                                                                 Best Local Similarity 43.4%;
Matches 155; Conservative B
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GVFVMETLSVMIQVASFKLT----GRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVI 348
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| GVFFVETLSVSMQVANFKISKKLYGEGRRIFLMAPLHHHFQLKGWAEQKIVIRFWIISIL 356
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                                                                                                                                                                                                                                                                                                1 MLLLLABYLQQFYK--GFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVR
                                                                                                                                                                                                                                                                                                                                                                                                59 NDGPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYR
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NCB TaxID=173;
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Los Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB011377; AAN49247.1; -
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0008663; P:phospho-"acetylmuramoyl-pentapeptide-trans...;
R GO; GO:0016740; P:transferase activity; IEA.
R GO; GO:0006629; P:lipid metabolism; IEA.
R GO; GO:0006629; P:peptidoglyvan biosynthesis; IEA.
R InterPro; IRR000715; Glyco,trans 4.
R InterPro; IRR0015; Glyco,trans 4.
R InterPro; IRR00524; PNAcPpept_trans.
R Fan, PROSS; Glycos_transfe_4; 1.
R TIGREAMS; TIGRR00445; max; 1.
R PROSITE; PS01347; MRAY_1; 1.
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                                                                                                                                                                 45.1%; Score 828; DB 16; Length 3
43.3%; Pred. No. 3.4e-52;
ive 78; Mismatches 117; Indels
                                                                       PROSITE; PS01347; MRAY_1; 1.
PROSITE; PS01348; MRAY_2; 1.
Transferase; Complete prome.
SEQUENCE 368 AA; 40769 MW; 70F16FA3A3DE4F6A CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide- transferase (MRXI OR LA2048.
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InterPro; IPR003524; PNAcPpept trans.
Pfam: PF00953; Glycos transf 4; 1.
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                               Pfam; PF00953; Glycos_transf_
TIGRFAMs; TIGR00445; mraY; 1
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01-MAR-2003 ('
01-MAR-2003 ('
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TEXALNANCE INCO N.A.

SEQUENCE FROM N.A.

TEXALNANCE 11168

WEDLINE=20150912; PubMed=10688204;

MEDLINE=20150912; PubMed=10688204;

A PATKHIL J., WEN B.W., Mungall K., Ketley J.M., Churcher C.,

A Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

A Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Mitchead S., Barrell B.G.,

Mitchead S., Barrell B.G.,

The genome sequence of the food-borne pathogen Campylobacter jejuni

Reveals hypervariable sequences.";

Teveals hypervariable sequences.";

Teveals hypervariable sequences.";

Nature 403:665-66812000).

FIR, Gall387; GB1387.

GO: GO: 00016020; C:membrane; IEA.

BR GO: GO: 00016020; C:membrane; IEA.

GO: GO: 00016020; C:membrane; IEA.

GO: GO: 00016020; P: hipid metabolism; IEA.

GO: GO: 00016022; P: phospho-Nacetylmuramoyl-pentapeptide-trans. .; IEA.

GO: GO: 00016022; P: phospho-Nacetylmuramoyl-pentapeptide-trans. .; IEA.

InterPro; IPRO03715; Glyco, trans f. 4.

InterPro; IPRO03524; PNAcPpept Lans.

BR Faan; PR00853; Glycos trans f. 4.

ITGRFAMS; TIGRO0445; max'; 1.

REPROSITE; PS01134; MRAY 1; 1.

Complete proteome.

SW SEQUENCE 1553 AA; 39239 MW; REBBCFG4F1061C95 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHLSKKGTPTMGGALILTALAISTLLWADLSNRYYWVVLVVTLLFGAIGWVDDYRKVIEK 123
                                                                                                                                                                                                                                                                                          SHEIKKGTPTWGGLLIIGSLLISVILWGNLKNPNVILLSVFSLSFSVLGFADDYMKSVKK 123
                                                                                                                                                                                                                                                                                                                                                                                        124 NSRGLPSRWKYFWQSVFG-IGAAVFLYMTAETPIE-----TTLIVPMLKSVEIQLGIF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 IKGGMRARTKFILSILISFIFCILFFYYTGTTGQTGKISFQLTDLFFPFIKGPVIALGII 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVVLTYFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPG 235
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                                                                                                         8 YLQQFY----KGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRNDGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NOBT_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)
MRAY OR CJ0433C.
                                     12;
   ; Pred. No. 1.5e-51;
66; Mismatches 120; Indels
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       45.8%;
                                     167; Conservative
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Best Local Similarity
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                                                                                                                                              FWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLTYFVIVGSSNAVNLT 194
                                                                                                                                                                                                         195 DGLDGLAIMPTVMVAGALGIFCYLSGNVKFABYLLIPNVPGAGELIVFCAALVGAGLGFL 254
                                                                                                                                                                                                                                                                    WENTYPAQVEMGDVGALALGAALGTIAVIVRQEJVLFIMGGVFVMETLSVMIQVASFKGJT 314
                                                                                                                                                                                                                                                                                                                                    248 WYNCYPAQVFWGDSGSLALGGFIGFLAVISKNEILLLIGFVFVLETVSVILQVGSFKIF 307
                                                              75
                                                                                           10 YAFFTYISVRAGFAFFIALCLSLFLMPKFITWAKAKNASQPIYEYAPETHKTKCHTPTMG
                                                            16 FGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRNDGPQSHLSKKGTPTWG
                                Gaps
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42.6%; Score 782.5; DB 16; Length 353;
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                  44.8%; Pred. No. 6.4e-49;
cive 70; Mismatches 118; Indels
   Query Match
Best Local Similarity 44.8*
Matches 155; Conservative
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Search completed: May 7, 2004, 08:40:32 Job time : 58 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 7, 2004, 08:37:37 ; Search time 18 Seconds (without alignments) 1041.403 Million cell updates/sec Run on:

US-10-089-787-2 1837 1 MillaeylqQpykGFGVPQ......RFWIITVILVLIGLATLKLR 360

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

O9zcw0 rickettsia	Psy436 Duchnera ap	066465 aquitex aeo	Q8rdq0 fusobacteri	Q44776 borrelia bu	Q9zlyl helicobacte	025235 helicobacte	Q9k9s6 bacillus ha	007322 staphylococ			Q8cpk7 staphylococ
MRAY RICPR	MRAY_BUCBP	MRAY AQUAE	MRAY_FUSNN	MRAY BORBU	MRAY HELPJ	MRAY HELPY	MRAY BACHD	MRAY STAAM	MRAY STAAW	MRAY_BACSU	MRAY_STAEP
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361	340	359	361	351	353	353	325	321	321	324	321
48.3	47.6	46.5	44.6	44.2	38.6	38.6	36.5	35.5	35.5	35.4	34.8
887.5	875	853.5	819	812.5	709.5	708.5	671	652	652	651	639
34	32	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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us-10-089-787-2.rsp
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GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phospho-N-acetylmuramcyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-MurNAc-pentapeptide phosphotransferase)
MRAY OR PP1334.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
MEDLINE=22423060; PubMed=12534463;
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J., Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
                                                                                     Cell division; Transferase; Transmembrane;
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0
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Bacteria, Profeobacteria, Gammaproteobacteria, Pseudomonadales
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                           Length 360;
                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                           R -> P (IN REF. 1).
E -> D (IN REF. 1).
DE8BEE7557091CB3 CRC64;
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99.4%; Pred. No. 2.1e-122;
tive 1; Mismatches 1;
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POTENTIAL.
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Matches 358; Conserv
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MGAY_PSEPK
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Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
Rraser C.M.;
Rraser C.M.;
Tomplete genome sequence and comparative analysis of the
metabolically versatile Fseudomonas putida KT2440.";
The Environ. Microbiol. 4:799-808 (2002).
L. Environ. Microbiol. 4:799-808 (2002).
C. I- FUNCTION: First step of the lipid cycle reactions in the
Diosynthesis of the cell wall peptidoglycan (By similarity).
C. I- ALALYTIC ACTIVITY: UDPMUTZAC (0yl-L-Ala-gamma-D-Glu-L-Lyse-D-Ala-D-Ala) - diphosphate = UMP + MurzAc (0yl-L-Lyse-D-Ala-D-Ala) - diphosphoundecaprenol.
C. I- STMILMAR LOCATION: Integral membrane protein (By similarity).
C. I- STMILMATTY: Belongs to the glycosyltransferase family 4. Mray
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DR HAMAP; MF 00038; -; 1.

DR InterPro; IPR000715; Glyco_trans_4.

DR PEdm; FP00933; Glycoo_trans_f 4; 1.

DR PROSITE; PS01347; MRAY_1; 1.

DR PROSITE; PS01347; MRAY_1; 1.

KW Peptidoglyvan synthesis; Cell division; Transferase; Transmembrane;

TRANSMEM 71 90 Potential.

TRANSMEM 71 90 Potential.

TRANSMEM 71 156 Potential.
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91B911C3B4118DE6 CRC64;
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Gaps

Indels

Pred. No. 1.2e-110; ', Mismatches 20;

89.7%; Fil. 17;

323; Conservative

Best Local Similarity Matches 323; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Phospho-N-acetylmuramcyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-MARAC-pentapeptide phosphotransferase).
MRAY OR PSPTO4411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell division; Transferase; Transmembrane;
                                                                                                                                                                                                                                        Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacee; Pseudomonas.
NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 360;
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CF79F93DC0A8CD66 CRC64;
                                                    360 AA.
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HAMAP; MF 00038; -; 1.
Interbro; IPR000715; Glyco_trans_4.
Pfam; PF00553; Glycos transf_4; I.
PROSITE; PS01347; MRAV_1; 1.
PROSITE; PS01346; MRAY_2; 1.
PROSITE; PS01346; MRAY_2; 1.
Complete proteome 21 43 Potential
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RN SEQUENCE FROM N.A.

REATURE 20020145; PubMed=12024217;

RX ABDLINE=20202145; PubMed=12024217;

RX ABDLINE=20202145; PubMed=12024217;

RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluye M.A., Almeida N.F.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluye M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Beartollini M.C., Camargo L.B.A.,

RA Alves L.M.C., do Amaral A.M., Eartollini M.C., Camargo L.B.A.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M. N., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Estuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali B.C., Machado M.A., Madeira A.M. B.N., Martinez-Rossi N.M.,

RA Locali B.C., Machado M.A., Madeira A.M. B.N., Martinez-Rossi N.M.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., Ae Souza R.F.,

RA Prindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M.P.,

ROMPATION: First step of the lipid cycle reactions in the blosynthesis of the cell wall peptidoglycan (By similarity).

C. I. FUNCTION: First step of the lipid cycle reactions in the blosynthesis of the cell wall peptidoglycan (By similarity).

C. I. SUNGELDUAR LOCATIVITY: Indeparal membrane protein (By similarity).

C. I. SUNGELDUAR LOCATION: Integral membrane protein (By similarity).

C. I. SIMILARITY: Belongs to the glycosyltransferase family 4. Mrax

C. I. SUNGELDUAR LOCATION: Litesparal membrane family 4. Mrax

C. I. SUNGELDUAR LOCATION: Litesparal membrane family 4. Mrax

C. I. SUNGELDUAR LOCATION: Litesparal membrane family 4. Mrax
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                                                                                                                      61 GPQSHLSKSGTPTMGGALILSSIGISTLLWADLSNRYVWVJLVTFLFGAIGWVDDYRKV
                                                                                                                                                                                           121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT
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                                                                                                                                                                                                                                                                                                                                                                                                          301 TLSVVIQVASFKLTGRRVFRYAPIHHHFELKGWPEPRVIVRFWIITVILVLIGLATLKLR
                                                                                             61 GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
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1 MILLIAEYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-MurNAc-pentapeptide phosphotransferase).

MARY OR XAC077.
Xanthomonas axonopodis (pv. citri).
Xanthomonas axonopodis (sy. citri).
Xanthomonadaceae; Xanthomonas.
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MILLLAEYLQGYYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLGIPQIGQAVRND
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-MurNac-pentapeptide phosphotransferase).
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                       Cell division; Transferase; Transmembrane;
                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                    63; Indels
                                                                                                                                                                                                                                                                                              BC44B2A5027348AB CRC64;
                                                                                                                                                                                                                                                                                                                72.5%; Score 1331.5; DB 70.4%; Pred. No. 1.6e-87; ive 43; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AA.
                                                                                                 HAWAP; MF_00038; -; 1.
InterPro; IRR000115; Glyco_trans_4.
InterPro; IRR000115; Glyco_trans_4.
InterPro; IRR003524; PMcPpept_trans.
Fram; PP00953; Glycos_transf_4; 1.
TIGREAMs; TIGR00445; mraY; 1.
PROSITE; PS01344; MRAY_2; 1.
PROSITE; PS01348; MRAY_2; 1.
Peptidoglycan synthesis; Cell division;
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POTENTIAL.
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                                                                                        EMBL; AE011708; AAM35665.1; -.
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39626 MW;
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Best Local Similarity 70.4%
Matches 254; Conservative
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2003
3390
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AAA;
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TRANSMEM 21
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MRAY_XANCP
ID MRAY_XANCP
AC Q8PCK2;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN-ATCC 33913 / NCPPB 528;

KMEDINES-2022145; PubMed-12024217;

MEDINES-2022145; PubMed-12024217;

A lucagio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A luces L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Caracili R.M.B., Coutlinho L.L., Cursino-Santos J.R., El-Dorry H.,

Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Katajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing
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Nature 417:459-463 (2002).

-!- FUNCTION: First step of the lipid cycle reactions in the biosynthesis of the cell wall peptidoglycan (By similarity).

-!- CARLYTIC ACTIVITY: UDPMurZAG(oyl-L-Ala-agamma-D-Glu-L-Lys-D-Ala-D-Glu-L-Lys-D-Ala-D-Glu-L-Lys-D-Ala-D-Ala) + diphosphoundecaprenol.

-!- PATHWAY: Peptidoglycan biosynthesis.

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SUBCELLULAR Belongs to the glycosyltransferase family 4. MraY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
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PROSITE; PS01348; MRAY_2; 1.
Peptidoglycan synthesis; Cell division; Transferase; Transmembrane; Complete proteome.
TRANSMEM 21 43 POTENTIAL.
Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 1327.5; DB 1; Length 361; ; Pred. No. 3.1e-87; 44; Mismatches 64; Indels 1;
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PF547C44E4FD21B8 CRC64;
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InterPro; IPR000715; Glyco trans 4.
InterPro; IPR003524; PNAcPpept_trans.
Pfan; PP00953; Glycos transf 4; 1.
TIGRFAMS; TIGR00445; mraY; 1.
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Best Local Similarity 69.8
Matches 252; Conservative
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361 AA;
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X MEDINES-2297686; PubMed=12368813;

Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

A Meyer T., Tsapin A., Scott J., Beanan M., Brinkec L., Daugherty S.,

DeBoy R.T., Dodson R.J., Umayam L.A., White O., Wolf A.M.,

A Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,

A Manathervan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

A Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

Redonne sequence of the dissimilatory metal ion-reducing bacterium

Shwanella oneidensis.";

Net. Biotechnol. 20:1118-1123(2002).

I FUNCTION: First step of the libid cycle reactions in the
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                                                                                                                                                                                                                                                                                                                                                                          1 MLVYLAEYLTQFYSGFNVFSYVTFRAILGLMTALVFCLWWGPKMIRRLQTLQIGQVVRSD
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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53B2A2BAEF6B6FE4 CRC64;
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15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
16-WAR-2004 (Rel. 43, Last annotation update)
Murikanoplo-Pentapeptide-transferase (BC
Murikanopentapeptide phosphotransferase)
                                                                                                                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                       71.4%; Score 1312; DB 1; 69.2%; Pred. No. 3.9e-86; ive 44; Mismatches 67;
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nes 249; Conservative
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TRANSMEM 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                      ETLSVMIQVASFKLTGKRVPRMAPIHHHFELKGWPEPRVIVRFWIISVVLVLIGLATLKV 360
                                                                                                                                                                                                                                                                         IVFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVM 299
                                                                                                                                                                                                                                                                                                                                                   ETLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKL 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: First step of the lipid cycle reactions in the biosynthesis of the cell will peptidoglycan (By similarity).
-!-CATALYTIC ACTIVITY: UDPMARZAC(Oyl-L-Ad-gamma-D-Glu-L-Lyg-D-Ala-D-Ala) + undecaprenyl phosphate = UMP + Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lyg-D-Ala-D-Ala-D-Ala-D-Ala-Gamma-D-Glu-L-Lyg-D-Ala-D-Ala-Gamma-D-Glu-L-Lyg-D-Ala-Gamma-D-Glu-L-Lyg-D-Ala-Gamma-D-Glu-L-Lyg-D-Ala-D-Ala-Gamma-D-Glu-L-Lyg-Boridoglycan biosynthesis.
-!-PATHWAY: Peptidoglycan biosynthesis
-!-SAUGELLUAR LOCATION: Integral membrane protein (By similarity).
-!-SIMILARITY: Belongs to the glycosyltransferase family 4. MraY
                                                                                                                                                                                                                 MLLELARWLQQLESLFGLFNYLTFRGILAALTALFLSLWMGPAVIRKLAQFKGGQPIRQD
                                     GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
                                                            121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQL-GIFFVVL
                                                                                                                                                                                          TYFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)
MuxNAc-pentapeptide phosphotransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gammaproteobacteria; Alteromonadales;
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InterPro; IRR000715; Glyco_trans_4.
InterPro; IRR000715; RNAcPpept_trans.
Pfam; PF00953; Glycos_transf_4; 1.
IIGRFAMS; TIGR00445; mraf; 1.
PROSITE; PS01347; MRAY_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shewanella violacea.
Bacteria; Proteobacteria; Gam
Alteromonadaceae; Shewanella.
NCBI_TaxID=60217;
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MRAY SE Q9F1N3;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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biosynthesis of the cell wall peptidoglycan (By similarity).
--- CATALYITC ACTIVITY: UDPMLZA6(cyl-L-Ala-agamma-D-Glu-L-Lys-D-Ala-D-Ala) + undecaprenyl phosphate = UMP + MurZAc(cyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol.
--- PATHMARY: Peptidoglycan biosynthesis.
--- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
--- SIMILARITY: Belongs to the glycosyltransferase family 4. MraY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLVXLAEYLTRFHTGFNVFSYVTFRAILGLLTALMFSLWWGPKLIERLQLMQIGQVVRND
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InterPro; IPR003154; FNAcPpept_trans_4.
InterPro; IPR003154; FNAcPpept_trans.
Pfam, PR00515; Glycos_transf_4; 1.
FIGRPAMS, TIGR00445; mray_i 1.
PROSITE; PS01347; MRAY_2; 1.
PROSITE; PS01348; MRAY_2; 1.
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CF447768C8F73217 CRC64;
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360 AA;
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361 AA.

STANDARD;

MRAY XYLFA ID MRAY XYLFA AC Q9PF83;

RESULT 8

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STRAINE=2036517; PubMed=10910347;

A Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Simpson A.J.G., Reinach F.C., Arruda P., Boyloston A.J.G., Baptiste A.B., Alvaerone M.B., Bordone E.M., Bordin S., Bove G.M., Briones M.R.S., Barros M.H., Bonacocots E.D., Camargo D.E., Carraro D.M., Carrer H., Colatto N.B., Colombo C., Cotar F.F., Carraro D.M., Carrer H., Colatto N.B., Colombo C., Cotar F.F., Costa M.C.R., Costa M.C.R., Colatul A.D., Ferreira A.J.S., Ferreira V.C.A., Ferro C.M., Ranchor D.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Radina J.B., Franca S.C., Franco M.C., Ferreira V.C.A., Ferro J.A., Radina G.H., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Racincado M.A., Madeira M.B., Madina M.H.S., Marino C.L., Anderica M.B., Marina E.A.L., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Matcha B.A., Machala M.A., Macinemto A.L., Nonteiro-vitorello C.B., Mono D.H., Nagai M.A., Nascimento A.L., Nonteiro-vitorello C.B., Anderica M.C., de Oliveira R.C., Palmieri D.A., Perguero J.B., Anderica M.C., de Coliveira M.C., de Sola A.J., Genes A.J., Ade Salva M.A., Verjovski-Almeida S.M., Tsulako M.L., Ade Solva A.J., Truffi D., Tagi S.M., Tsulako M.L., Ade Solva A.J., Thuffi D., Tagi S.M., Tsulako M.L., Ade Solva M.A., Zatz M., Meidanis M.S., Salva M.A., The Genome Sequence of the plant pathogen Xylella fastidiosa.";

Rule Genome Sequence of the plant pathogen Xylella fastidiosa.";

Rule Genome Sequence of the plant pathogen Xylella fastidiosa.";

Rule Genome Sequence of the plant pathogen Xylella fastidiosa.";

Rule Genome Sequence of the plant pathogen Xylella fastidiosa.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the glycosyltransferase family 4. MraY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptidoglycan synthesis; Cell division; Transferase; Transmembrane;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phospho-N-acetylmuramcyl-pentapeptide-transferase (EC 2.7.8.13)
MurNac-pentapeptide phosphotransferase).
                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
NCBL_TaxID=2371;
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HAWAP; MF_00038; -; 1.
InterPro; IPR000715; 01yco_trans_4.
InterPro; IPR003524; PNACPPept_trans.
Pfan; PP00953; G1ycos_transf_4; 1.
TIGRPAMs; TIGR00445; mraY; 1.
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PROSITE: PS01348; MRAY 2;
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                                                                                                                                           Xylella fastidiosa.
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Thu May 13

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM S.A.

SEQUENCE FROM S.A.

MACHINE-ZED08454; PubMed=12620735;

A Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

A Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholarae.";

Lancet 361:743-749(2003)

C -!- FUNCTION: First step of the lipid cycle reactions in the biosynthesis of the cell wall peptidoglycan (By similarity).

C -!- CATALYTIC ACTIVITY: UDPMur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala) -diphosphoundecaprenol.

Glu-L-Lys-D-Ala-D-Ala) -diphosphoundecaprenol.

C -!- PATHWAY: Peptidoglycan biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GPKWHFSKAGTPTMGGSLILMTVTLSVLLWGDLRNRYVWLVLVVWLAFGAIGWYDDWIKL 120
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                                                                                                                                                                                                                                                                                                                                                                      121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQL-GIFFVVL 179
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-MurNAc-pentapeptide phosphotransferase)
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                 Score 1296.5; DB 1; Length 361;
Pred. No. 4.9e-85;
3; Mismatches 71; Indels 1;
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Bateria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
VGBI_TaxID=670;
                                                                                                                                   83A40BDD66F990CF CRC64;
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Matches 246; Conservative
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MRAY VIBPA
AC 087857; DEPA
DT 10-0CT-2003
DT 10-0CT-2003
DT 10-0CT-2003
DE PROSPIO-N-ac
DE MUNNAC-PENTA
GN WRAY OR VP04
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SUBCELLULAR LOCATION: Integral membrane protein (By similarity) SIMILARITY: Belongs to the glycosyltransferase family 4. MraY subfamily.
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MRAY_XYLFT

AC (037AF),

DT 10-0CT-2003 (Rel. 42, Created)

DT 10-0CT-2003 (Rel. 42, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last sequence update)

DT 10-0CT-2003 (Rel. 42, Last annotation update)

DF 10-0CT-2003 (Rel. 42, Last sequence update)

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Matches 243; Conservative
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                                                                  240 IVFCAALVGAGLGFLWFNTYPAQVFWGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVM 299
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                                                                                                             SEQUENCE FROM N.A.

MEDLINE=22421311; PubMed=12533478;

MEDLINE=22421331; PubMed=12533478;

MEDLINE=22421331; PubMed=12533478;

MEDLINE=22421331; PubMed=12533478;

MIYAKI CY., Furlan D.R., Genoargo L.E.A., da Silva A.C.R., Moon D.H.,

Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

A Goldman M.H.S., Goldman G.H., Lemos M.V., BI-Dorry H., Tsai S.M.,

Carrer H., Carraro D.M., Goldine R.C., Numes D.E., Siqueira W.J.,

Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

da Cunha A.F., Fenille R.C., Ferro J.Y., Sassaki F.T., Sena J.A.D.,

de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

Kitajima J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol., 185:1018-1026(2003).

J. Bacteriol., 185:1018-1026(2003).

J. FUNCTION: First step of the lipid cycle reactions in the biosynthesis of the cell wall peptidoglycan (By similarity).

J. CATALYTIC: UDPMATZAC(0y1-L-Ala-agamma-D-Glu-L-Lys-D-Ala-D-Ala) + undecaprenyl phosphoundecaprenol.

J. PATHWAY: Peptidoglycan biosynthesis.

J. SAHWAY: Peptidoglycan biosynthesis.

J. SUBCELULAR LOCATION: Integral membrane protein (By similarity).

J. SIMILARITY: Belongs to the glycosyltransferase family 4. Mray
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xylella.
NCBI_TaxID=183190;
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HAMAP, MF 00038; -; 1
InterPro; IPR000715; Glyco_trans_4.
InterPro; IPR000554; PNRcPpept_trans.
Pfam, PF0055; Glycos_transf_4; 1.
PROSITE, PS01347; MRAY_1; 1.
Peptidoglycan synthesis; Cell division; Tracomplete proteome.

TRANSMEM 71 90 Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1] STRAINGE FROM N.A. Serotype O1; STRAINGE FROM N.A. SEQUENCE FROM N.A. MEDLINE-20406833; PubMed=10952301; MEDLINE-20406833; PubMed=10952301; Melson R.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodsson R.J., Haft D.H., Hickey B.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Gill S.R., Nelson K.E., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406 4477-483 (2000).

Nature 406 477-483 (2000).

-!- FUNCTION: First step of the lipid cycle reactions in the biosynchesis of the cell wall peptidoglycan (By similarity).

-!- CATALYTIC ACTIVITY: UDPMur2Ac (oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Glu-L-Lys-D-Ala-D-Glu-L-Lys-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-Ala-D-A
                                                                                          -1- PATHWAY: Peptidoglycan biosynthesis.
-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: Belongs to the glycosyltransferase family 4. MraY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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HAMAP; MP_00038; -; 1.
InterPro; IPR000715; Glyco_trans_4.
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   361
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61 GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120 GPKWHFSKAGTPIMGGSLILMTVTLSVLLMGDLRNRYVWLVLVVMLAFGAIGWYDDWIKL 120

67.98;

Best Local Similarity 67.9 Matches 245; Conservative

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Choy H.E.,
"Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: First step of the lipid cycle reactions in the biosynthesis of the cell wall peptidoglycan (By similarity).
-!- CATALYTIC ACTIVITY: UDPMLZAG (Oyl-L-Ala-gamma-D-Glu-L-Lyg-D-Ala-D-Ala) + undecaprenyl phosphate = UMP + Mur2Ac(oyl-L-Ala-gamma-D-
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amontation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase (BC 2.7.8.13) (UDP-MurNAC-pentapeptide phosphotransferase).
Wibrio vulnificus.
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                                                                                                                                                           Transferase; Transmembrane;
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Vibrionaceae; Vibrio.
VCBI_TaxID=672;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
81727653AF899E53 CRC64;
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66.9%; Pred. No. 1e-84;
ive 51; Mismatches 6
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InterPro, IPR003524; PNAcPpept trans.

PEGM; PF0093; Glycos_transf_4; 1.

PROSITE; PS01347; MRAY_1; 1.

PROSITE; PS01348; MRAY_2; 1.

PROSITE; PS01349; MRAY_2; 1.

TRANSMEM 74 93 POTENTIAL.

TRANSMEM 171 193 POTENTIAL.

TRANSMEM 237 256 POTENTIAL.

TRANSMEM 237 256 POTENTIAL.

TRANSMEM 289 311 POTENTIAL.

TRANSMEM 289 311 POTENTIAL.

TRANSMEM 289 311 TRANSMEM 289 311

TRANSMEM 289 311

TRANSMEM 289 311

TRANSMEM 289 311

TRANSMEM 289 311
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SEQUENCE FROM N.A.
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Best Local Simil
Matches 241; C
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MRAY VIBVA
AC QBDEX7;
DT 10-0CT-2
DE PHOSPIO-
DE PLOSPIO-
DE MINAC-PORTO
DE MINAC-PORT
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MRAY PASMU STANDARD; PRT; 360 AA.

AC P57816;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-PEB-2003 (Rel. 41, Last annotation update)

DF 28-PEB-2003 (Rel. 41, Last annotation update)

DF Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) (UDP-
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Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol.
-!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the glycosyltransferase family 4. MraY subfamily.
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HAMAP; MF_00038; -; 1.
InterPro; IPR000715; Glyco_trans_4.
InterPro; IPR00324; FWACPept_trans.
Pfam; PP00953; Glycos_transf_4; 1.
TIGREAMS; TIGR00445; mrax; 1.
PROSITE; PS01349; MRAY_1; 1.
PROSITE; PS01348; MRAY_2; 1.
Peptidoglycan synthesis; Cell division; Transmanner
TRANSMEM 74 93 POTENTIAL.
TRANSMEM 74 93 POTENTIAL.
TRANSMEM 77 114 POTENTIAL.
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nes 241; Conservative
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                                                                                        May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Scil. U.S.A. 9813460-3465(2001).
-!- FUNCTION: First step of the lipid cycle reactions in the biosynthesis of the cell wall peptidoglycan (By similarity).
-!- CATALYTIC ACTIVITY: UDPMArZAc(cyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala) + undecaprenyl phosphate = UMP + MurZAc(cyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala)-diphosphoundecaprenol.
-!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SUBCELLULAR Belongs to the glycosyltransferase family 4. MraX
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                            Gammaproteobacteria; Pasteurellales;
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B9BED1987FEDBD53 CRC64;
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MurNAc-pentapeptide phosphotransferase)
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                                                                        STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
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                         Bacteria, Proteobacteria, Gal
Pasteurellaceae, Pasteurella
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Matches 237; Conserv
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(See http://www.isb-sib.ch/announce/
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                                           R BMBL; AE016755; AAN78603.1; --
R RMBL; AE016755; AAG54391.1; --
R EMBL; AE00185; AAG54391.1; --
R EMBL; AP00250; BAB33514.1; --
R PIR; C9540; C95440;
R PIR, C95640; C90640; --
R InterPro; IPR00715; Glyco_trans_4.
R InterPro; IPR003524; PNAcPpept_trans.
R INTERPOS) TGR00445; mrax; 1:
R PROSITE; PS01349; MRAY_1; 1.
R PROSITE; PS01349; MRAY_1; 1.
R PROSITE; PS01349; MRAY_2; 1.
M PEPLIGOSIVCAN SYNTHESIS; Cell division; Transmembrane; M Complete proteome.
TRANSMEM 19 PERIPLASMIC (BY SIMILARITY).
TRANSMEM 19 PERIPLASMIC (BY SIMILARITY).
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51; Mismatches 70; Indels
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CYTOPLASMIC (BY SIMILARITY).

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RESULT 15 MRAY\_ECOLI ID MRAY\_ECOLI AC P15876;

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SPECIES=E.coli, STRAIN=K12,
MEDLINE=79082893; PubMed=215212;
Geis A., Plapp R.;
"Phospho-N-acctylmuramcyl-pentapeptide-transferase of Escherichia coli
K12. Properties of the membrane-bound and the extracted and partially
purified enzyme.";
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"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
"Ltrough comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phospho-N-acetyImuramoyl-Pentapeptide-transferase (EC 2.7.8.13) (UDP-
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIESE.Coli; STRAIN=K12;
MEDLINE=90192099; PubMed=2179861;
Ikeda M., Wachi M., Ishino F., Matsuhashi M.;
"Nucleotide sequence involving murb and an open reading frame ORF-Y
spacing murf and ftew in Becherichia coli.";
Nucleic Acids Res. 18:1058-1058(1990).
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SEQUENCE E.OMI, TALAIN=KI2 / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-S.fleaneri, STRAIN-2457T / ATCC 700930 / Serotype 2a, MEDLINE-22590274; PubMed=12704152; Met J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Met J., Goldberg M.B., Burland V., Venkatesan M.M., Dang W., Met J., Goldberg M.B., Burland V., Venkatesan M.M., Darling A., May B., Perra N.T., Payre S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Runyen-Janecky L.J., Zhou S., Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
                                                                                                                                                                                                                                     Shigella flexneri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
Notel_TaxID=562, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SERCIES=E.coli; STRAIN=K12;
MEDLINE313977; Pubmed=1630901;
Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
Isono K., Mizobuchi K., Nakata A.;
"Systematic sequencing of the Escherichia coli genome: analysis the 0-24 min region.";
Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                   MurNac-pentapeptide phosphotransferase).
MRAY OR MURX OR B0087 OR SF0084 OR S0086.
Escherichia coli, and
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                                                                                                                                                                                              POPOLOGY.

SPECISS=E.coli;

MEDLINE=20022370; PubMed=10564498;

MEDLINE=20022370; PubMed=10564498;

A Bouhss A., Mengin-Lecreulx D., Le Beller D., Van Heijenoort J.;

"Topological analysis of the mray protein catalyzing the first
membrane step of peptidoglycan synthesis.";

MOI. Microbiol. 34:576-585(1999)

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MOI. Microbiol. 34:576-585(1998)

MOI. Microbiol. 34:576-585(1998)

MOI. Microbiol. 34:576-585(1998)

MOI. MICROBIOLOGY

MOI. Microbiol. 34:576-585(1998)

MOI. Microbiol. 34:576-585(1988)

MOI. Microbiol. 34
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EcoGene; Ed10604; mrax.
HAMAPP MF 00038; -1, 1.

InterPro; IPR003524; PNAcPpept trans 4.

InterPro; IPR003524; PNAcPpept trans.

Pfam; PF00953; Glycos transf 4; 1.

IIGRPAMS; TIGR00445; mray; 1.

PROSITE; PS01347; MRAy 1; 1.

PROSITE; PS01348; MRAy 2; 1.

PROSITE; PS01348; MRAY 2; 1.

PROSITE; PS01348; MRAY 2; 1.
MEDLINE=91123172; PubMed=1846850; Ishino F., Matsuhashi M.; Tkeda M., Wachi M., Jung H.K., Ishino F., Matsuhashi M.; pentanetichia coli mraY gene encoding UDP-N-acetylmuramoylpentapeptide; undecaprenyl-phosphate phospho-N-acetylmuramoylpentapeptide transferase."; J. Bacteriol. 173:1021-1026(1991).
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EMBL; X55034; CAA38864.1; -.
EMBL; D10483; BAB96655.1; -.
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                                                                                                                               61 GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
                                                                                                                                                 1 MLVWLAEHLVKYYSGFNVFSYLTFRAIVSLLTALFISLWMGPRMIAHLQKLSFGQVVRND
                                                                                                                                                                                                                                                      YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI
                                                                                                                                                                                                                                                                                 181 YFVIVGTGNAVNLTDGLDGLAIMPTVFVAGGFALVAWATGNMNFASYLHIPYLRHAGELV
                                                                                                                                                                                                                                                                                                                241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME
                                                                                                                                                                                                                                                                                                                                                                             301 TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR
                                                                  1 MILLLABYLOOFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND
                                        Gaps
                                        ö
         Length 360;
                                        70; Indels
         Score 1268; DB 1;
Pred. No. 5.1e-83;
69.0%; Scor.
66.4%; Pred. No. s.r.
61; Mismatches
11; Mismatches
                                        Conservative
         Query Match
Best Local Similarity
Matches 239; Conserv
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Search completed: May 7, 2004, 08:38:11 Job time : 19 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 7, 2004, 08:37:38 ; Search time 21 Seconds (without alignments) 1648.998 Million cell updates/sec

US-10-089-787-2 1837 1 MLILLAEYLQQFYKGFGVFQ......RFWIITVILVLIGLATLKLR 360 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		ð			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	1	ŀ		1	1	!
-	82	σ.	•^	7	9	phospho-N-acetylmu
71	٠,	ö	36	7	B82763	ď
m	29	ö	36	~	8	phospho-N-acetylmu
4	26	6	36	М	S)	phospho-N-acetylmu
ιO	26	6	36	7	54	hypothetical prote
Ψ	26	σ.	36	N	σ	hypothetical prote
7	1265	ω.	36	~	AE0068	phospho-N-acetylmu
8	26	ω.	36	N	51	phospho-N-acetylmu
σ	21	Ġ.	36	Н	A64185	phospho-N-acetylmu
10	10	φ,	36	~	0	phospho-N-acetylmu
11	60	φ.	36	0	817	phospho-N-acetylmu
12	44	4	36	7	AB3324	phospho-N-acetylmu
13	-	φ.	36	7	AB2834	hypothetical prote
14	917	49.9	36	7	F97611	phospho-N-acetylmu
15	'n.	φ.	35	7	G84955	phospho-N-acetylmu
16	。	8	36	~	F97813	hypothetical prote
17	۲.		36	7	E71664	phospho-n-acetylmu
18	e.	•	35	~	F70304	phospho-N-acetylmu
19	ά.		35	N	G70137	phospho-N-acety1mu
20		ų.	35	Ŋ	G81387	phospho-N-acetylmu
21	٩.	œ.	35	~1	B71930	phospho-n-acety1mu
22	œ.	œ,	35	н	E64581	phospho-N-acetylmu
23	S	'n	32	~	A89890	phospho-N-muramic
24	S	'n.	32	Н	C47691	phospho-N-acetylmu
25	3	4.	32	N	AE1329	phospho-N-acetylmu
26	3		32	7	AE1700	phospho-N-acetylmu
27	m	4.	36	~1	T34957	probable phospho-N
28	605.5	33.0	317	~	B97162	~
29	94.	32.4	w	7		phospho-N-acetylmu

phospho-N-acetylmu	probable murk prot	hypothetical prote	muramoy1-pentapept	phospho-N-acety1mu	muramoy1-pentapept	hypothetical prote	phospho-N-acetylmu	phospho-N-acety1mu	hypothetical prote	phospho-N-acetylmu	phospho-N-acetylmu	probable muramoyl-	phospho-N-acetylmu	hypothetical prote	phospho-N-acetylmu
Н83970	H70579	A87023	B86603	A81519	G72021	695039	A97910	S77076	D86733	E81736	E72402	D71474	F75346	T04929	C69198
(1)	N	N	N	~	~	7	7	-	01	7	Ŋ	N	~	~	-
47	329	359	349	349	349	326	326	365	329	35	302	336	312	236	351
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30.2				29.7	29.6			28.3							
.5 30.2	30.0	8 29.8				28.7	28.3	519 28.3	27.6	27.5		26.0	5 24.5	18.6	5 16.1

# ALIGNMENTS

RESULT 1 H83094 Phospho-N-acetylmuramcyl-pentapeptide- transferase PA4415 (imported] - Feeudomonas aerugi C;psecise: Pseudomonas aeruginosa C;pacession: H83094 R;Scorost, CK.; Phan, X.; Brody, L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Lim, S.; Lim, S.	Db 241 VFCAALVGAGIGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVWE 300  Qy 301 TLSVAIQVASFKLTCRRVFRAAPIHHFELKGWPDFRVIVRFWIITVLIGLATLKLR 360  Db 301 TLSVAIOVASFKLTGRRVFRAAPIHHFELKGWPERRVIVRFWIITVLVLIGLATLKLR 360
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R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. M. R.R.; Makelanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82081
A;Accession: Proliminary
A;Molecule type: DNA
A;Residues: 1-360 <HBI>
A;Residues: 1-360 <HBI>
A;Residues: 1-360 <HBI>
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                                                                                                                                                                                                                                                                                  C, Genetics
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     p82763
phospho-N-acetylmuramoyl-pentapeptide- transferase XF0795 [imported] - Xylella fastidios
C;Species: Xylella fastidiosa constitution 20-Aug-2000 #text_change 02-Sep-2000
C;Species: May22000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: B8273
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82763
A;Staus: Ppellminary
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B2763
A;Cross-references: GG:AR003919; GB:AE003849; NID:g9105675; PIDN:AAF8360E.1; GSPDB:GNO01
A;Authors: Foreira C; B-Dorry, H; Factincani, A.P.; Ferraira, A.J.S.
Bringson, A.J. GG: Reinach, F.C.; Arruda, P.; Arranca, S.C.; Franco, M.; Matchors: Anderira, A.M. B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Matchors: Anderira, A.M. B.N.; Matchors: Anderira, R.M.; Anderira, M.J.; Kenper, E.L.; Kitajima, J.P.; Krieger, V. B.C.; Franco, M.S.; Ferraira, M.J.; Kanper, E.L.; Kitajima, J.P.; Marino, C.L.; Marques, M.J.; Matchors: Anderira, M.J.; Kanper, B.L.; Matchors: M.J.; Matchors: Anderira, M.J.; Kanper, M.J.; de Oliveira, M.J.; A.C.; Franco, M.J.; A.C.; A.J.; A.C.; A.J.; A.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETLSVIIQVTSFKLIGKRVFRWAPIHHFBLKGWPEPRVIVRFWIISVVLVLVGLATLKV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPOSHLSKKGTPTMGGALILTALAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVBIQL-GIFFVVL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFABYLLIPNVPGAGEL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 1296.5; DB 2; Length
; Pred. No. 1.2e-90;
43; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 68.1%;
Matches 246; Conservative 4
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phospho-N-acetylmuramoyl-pentapeptide- transferase VC2404 [imported] - Vibr. C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001 C;Accession: H82081

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A,Cross-references: EMBL:D10483, NID:g216434; PIDN:BAA01352.1; PID:g216501
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9-2
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 10-58p-199 # Heequesion 10-5ep-1999 #text_change 01-Mar-2002
C;Accession: S08395; S40597; G64730
R;Ikeda, M.; Wachi, M.; Ishino, F.; Matsuhashi, M.
Nucleic Acids Res. 18, 1058, 1990
A;Fitle: Nucleotide sequence involving murD and an open reading frame ORF-Y spacing
A;Reference number: S08395; MUID:90192099; PMID:2179861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S08395
A;Molecule type: DNA
A;Residues: 1-360 <1KE>
A;Molecule type: DNA
A;Residues: 1-360 <1KE>
A;Residues: 1-360 <1KE>
A;Cross-references: EMBL:X51584; NID:g42058; PIDN:CAA35932.1; PID:g42059
B;Yura, T.; Mori, H.; Nagai, H.; Nagata, T.; Ishihama, A.; Fujita, N.; Isono, K.; submitted to the EMBL Data Library, December 1992
A;Description: Systematic sequencing of the Bscherichia coli genome: analysis of A;Reference number: 840531
A;Accession: §40597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VVCTAMVGAGLGFLWFNIYPAQVFMGDVGALALGGALGTIAVLVRQBFVLVIMGGVFVME
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                                                                                                                                                                                   Gaps
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                                                                                                               Length 360;
A;Gene: VC2404
A;Map position: 1
C;Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
                                                                                                                                                                                   68; Indels
                                                                                                                   Query Match 70.3%; Score 1292; DB 2; Best Local Similarity 66.9%; Pred. No. 2.7e-90; Matches 241; Conservative 51; Mismatches 68;
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A Molecule type: DNA
A, Residues: 1-360 < YUR>
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number: A64720; MUID:97426617; PMID:9278503 :: G64730 reliminary; nucleic acid sequence not shown; translation not shown	<pre>ily: phospho-N-acetylmuramoyl-pent: tch 69.0%; Score 1268</pre>
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ž,	Db 1 MLVWLAEHLVKYYSGENVFSYLTFRAIVSLLTALFISLWMGFRMIAHLQKLS Qy 61 GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLFGAIG Db 61 GPESHFSKRGTPTMGGIMILTAIVISVLLWAYPSNPYVWCVLVULVGYGVIC
H	Qy 121 IEKNSRGLPSRWKXFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQI 
rransmembrane #status predicted <tm4> rransmembrane #status predicted <tm5> rransmembrane #status predicted <tm6> rransmembrane #status predicted <tm7> ransmembrane #status predicted <tm8> ransmembrane #status predicted <tm8></tm8></tm8></tm7></tm6></tm5></tm4>	Qy 181 YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPN
transmembrane #status predicted <tm9> transmembrane #status predicted <tm10> 69.0%; Score 1268; DB 1; Length 360;</tm10></tm9>	241 241
DESL DOCAL SIMILATILY SO.4%; FIEL. NO. 1.06-88; MATCHES 239; CONSERVATIVE 51; MISMATCHES 70; Indels 0; Gaps 0; MATCHES 239; LALLABYLQQFYKGFGVFQYLTLRGILSVLTALSLSLMLGPWMIRTLQIPQIGQAVRND 60	Db 301 TLSVILQVGSFKLRGGRIFRMAPIHHHYELKGWPEPRVIVRFWIISLMLVEI
:    :                       :	RESULT 6
GPGSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVUVVVTLLFGAIGWVDDYRKV 120	C85491 hypothetical protein mray [imported] - Escherichia coli (strain O) C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14
IEKNSRGLPSRWKXFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180 :  :::   :         :     :::  VRKDPKGLIARWKXPRWSVIALGVAFALYLAGKOTPATOLVVPFFKDVMPOLGLFYILLA 180	sner,
	A; Title: Genome sequence of enterohemorrhagic Escherichia coli O1 A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Accession: C85491 A:Status: preliminary
	A;Molecule type: DNA A;Residues: 1-360 <sto> A;Cross-references: GB.AE005174; NID:g12512790; PIDN:AAG54391.1; A;Experimental source: strain O157:H7, substrain EDL933</sto>
TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGMPDPRVIVRFWIITVILVLIGLATLKLR 360	C;Genetics: A;Gene: mraY C;Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
מכ אאסדופרדאני	Query Match 69.0%; Score 1268; DB 2; Length 360 Best Local Similarity 66.4%; Pred. No. 1.7e-88; Matches 239; Conservative 51; Mismatches 70; Indels
oli (stra	
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C.Accession: C90640 R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	61 1
ZUUL genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and geno . A99629; MUID:21156231; PMID:11258796	Qy 121 ISRNSRQIPSRWKYFWQSGAAVELYMTAETPIETTIVVMLKSVEIQ
an Fy NA NA	
Residues: 1-360 <hay> Cross-references: GB:BA000007; PIDN:BAB33514.1; PID:g13359547; GSPDB:GN00154 Experimental source: strain 0157:H7, substrain RIMD 0509952</hay>	Qy 181 YEVIVGSSNAVNLTDGLDGLAIMPTVWVAGALGIFCYLSGNVKFABYLLIP 
	Qy 241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLF

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imported] - Escherichia coli (strain 0157:H7, substrain EDL93:
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Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08174; NID:g12512790; PIDN:AAG54391.1; GSPDB:GN00145; UWGP:Z00
ain O157:H7, substrain EDL933
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56.4%; Pred. No. 1.7e-88;
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9.0%; Score 1268; DB 2; Length 36.6.4%; Pred. No. 1.7e-88;
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A;Accession: AB0518
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-360 <PAR>
A;Residues: 1-360 <PAR>
A;Crosererences: GB:AL513382; PIDN:CAD01282.1; PID:g16501410; GSPDB:GN00176
C;Genetics:
A;Gene: STY0145
C;Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
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A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Recence number: AB0001; MUID:21470413; PMID:11586360
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Corss-references: GB:AL590842; PIDN:CAC89408.1; PID:g15978644; GSPDB:GN00175
C; Generics: A; Gene: mray
C; Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
C; Keywords: transferase
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AB0518
phospho-N-acetylmuramoyl-pentapeptide- transferase [imported] - Salmonella enterica subs
phospho-N-acetylmuramoyl-pentapeptide- transferase [imported] - Salmonella enterica subs
c;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
c;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0518
R;Parkhill, J: Dougan, G:; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
h. T:; Connerton, P:; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
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Accession: Action in Electron and Sequence not shown; You'll Sequence in Transferase (EC 2.7.8.13) - Haemophilus influenzae (5/5pecies: Haemophilus influenzae) (5/5pecies: Haemophilus Haemophil
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Query Match         66.2%; Score 1216; DB 1; Length 360;           Best Local Similarity 61.9%; Pred. No. 1.5e-84;         74; Indels 0; Gaps 0;           Matches 223; Conservative 63; Mismatches 74; Indels 0; Gaps 0;         0;           QY         1 MLLLABYLOQPYKGFGVFQYLTLRGILSVLTALSLSLWLGPWNIRTLQIPQIGQARND 60           Db         1 MLVMLABYLVRYTETTARNILTALFISLWIGFKVIKRLQILKFGGEVRND 60           CD         61 GPQSHISKKGTPTMGGALILTATIAISTLWADLSNYWVVLVYTLLFGAIGWVDDYRKV 120           CD         61 GPESHFAKKGTPTMGGANILTATIAISTLWADLSNYWVLLYTLLFGAIGWVDDYRKV 120           CD         61 GPESHFAKKGTPTMGGVMILFSIGVSTLLWANLANYNVLVCLFVLFGYGAIGFVDDFRKI 120	Db 240 VIPCTAMCGACLGFLWFNAYPAQVFMGDVGALALGAALGTVAVIVRQEFVLVIMGGLFVV 299  Qy 300 ETLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVLVLIGLATLKL 359  300 EAVSVMLQVGWYKKTKCRIFLMAPIHHHYBQKGWKETQVVVRFWIITIVLVLIGLSTLKI 359  Qy 360 R 360  Db 360 R 360
OY 121 IEKNSRGLPSBWKYFWGSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIOLGIFFVULT 180  121 TRKNTDGLIAAWKYFWGSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIOLGIFFVULT 180  QY 181 YFVIVGSSNAVNLTDGLDGLAIMPTWVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 240  DD 181 YFVIVGSSNAVNLTDGLDGLAIMPTAMAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 240  QY 241 VFCALVGAGLGFLWFNTYPAQVFMGDVAGAFALGANGTAVITRGGVFVWE 300  DD 241 VFCTAIVGASLGFLWFNTYPAQVFMGDVGALAGGALGTAVITRGGFLVINGGVFVVE 300  QY 301 TLSVMIQVASFKLTGRRVFRMADIHHHPELKGWPDPRVIVFFWIITVILULIGIAATKKR 360  DD 301 ALSVLLQVGSYKLTKQRIFRMAPIHHHFELKGWPEPRVIIFFWIISLMLVLMGLVTLKRR 360	RESULT 11 F8177 phosphore. Neisezia meningitidis C;Species: Neisezia meningitidis C;Date: 05-May-2000 #text_change 02-Feb-2001 C;Accession: F8177 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell R;Parkhill, J.; Achtman, M.; James, K.D.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, S.02-S06, 2000 A;Tutle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUD:20222556; PMID:10761919 A;Recession: F8177 A;Atatus: preliminary A;Cassidues: 1-360 -PAA. A;Cross-references: GB:AL162758; GB:AL157959; NID:G7380672; PIDN:CAB85284.1; PID:G7380694
2; Eseria mening Gherty, B.A.; Za, M. Ppuoli, R.; Ve ain MC58. 1; PID:9722564 2; 60 60 59 1120 119	A) Experimental source: serogroup A, strain 22491 C:Genetics: A;Genetics: A;Genetics: C;Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase Matches 210; Conservative 58.2
Db 120 VYXDPNGVSAKFOVWQSSVAIIASLALFYLAANSANNILIVPFFKQIALFLGVVGFLVL 179  Qy 180 TYFVIVGSSNAVNLTDGLDGLAIMPTVAVACALGIFCYLSGSNYKFARYLLIPNVPGAGEL 239  180 SYLTIVGTSNAVNLTDGLDGLATFPVVLVAAGLAIFAXASGHSQFAQYLQLPYVAGANEV 239  Qy 240 IVFCAALVGAGLGFLWFNYYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVM 299	RESULT 12 AB3324

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C; Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
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App834

hypothetical protein mraY [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: AB2834
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Kwod, D.W.; Setubal, J.C.; Raul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Reference number: AD3252; PMID:11756688
A;Reference: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-360 «KUR>
A;Coss-references: GB:AE008917; PIDN:AAL51757.1; PID:g17982496; GSPDB:GN00190
C;Genetics:
A;Gene: BME10576
A;Map possition: A;Map cossition: A;Map cossition: A;Map possition: Dioperfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
C;Keywords: transferase
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; WUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 VIKOSDKGFSGKARLGIEFLIAAIAAFTIMRAGOEFFSSSLTFPFVKQLVINLSWFFIPF
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4.2e-64;
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1.366 «KUR»
A; Cross-references: GB: AB008688; PIDN
A; Experimental source: strain C58 (Dv. C; Genetics:
A; Gene: mraY
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Matches 185; Conser
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                                                                               DOPOTHERKAGTETMGGLMILAGILGGSLLWGDLSNVYVVAVLMVTLGFGAIGFYDDYLK
                                                                                                                                                                                             120 VIEKNSRGLPSRWKYFWQSVFGI----GAAVFLYM---TAETP----IETTLIVPMLKS
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                                                             1 MLLLLAEYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQ-IGQAVRN
                                                                                                                                                                                                                                                              168 VEIQLGIFFVVLTYFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEY
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A;Map position: circular chromosome
C;Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
 Length 366;
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Query Match
Best Local Similarity 52.0%; Pred. No. 5.6e-62;
Matches 194; Conservative 53; Mismatches 106; Indels
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Best Local Similarity 52.0%
Matches 194; Conservative
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phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13) [imported] - Buchnera sg
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C;Abace : 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G84955
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUID:20445173; PMID:10993077
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49.8%; Score 915.5; DB 2; Length 357;
Best Local Similarity 46.2%; Pred. No. 7.1e-62;
Matches 166; Conservative 86; Mismatches 104; Indels 3
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A Statutus: preliminary
A Molecule type: DNA
A Residues: 1-357 <STO>
A COORDES TELENCES: GB:AP000398; GSPDB:GN00144
A Experimental source: strain APS
C Genetics: B 10219
C Genetics: B 10219
C Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
C Keywords: transferase
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354 GLALLGLATLKLR 366
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Search completed: May 7, 2004, 08:40:55 Job time : 22 secs

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May 7, 2004, 08:40:38; Search time 48 Seconds (without alignments) 2081.751 Million cell updates/sec
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1837
1 MILLLAEYLQQFYKGFGVFQ......RFWIITVILVLIGLATLKLR 360
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 12011, A Sequence 66653, A	Sequence 67901, A		Sequence 66896, A	Sequence 451, App	Sequence 10028, A	Sequence 56412, A	Sequence 77920, A	Sequence 76018, A	Seguence 75186, A	Sequence 14075, A	Sequence 11691, A	Sequence 55841, A
SUMMARIES	US-09-815-242-12011 US-10-282-122A-66653	US-10-282-122A-67901	US-10-282-122A-02/13	US-10-282-122A-66896	US-09-741-669-451	US-09-815-242-10028	US-10-282-122A-56412	US-10-282-122A-77920	US-10-282-122A-76018	US-10-282-122A-75186	US-09-815-242-14075	US-09-815-242-11691	US-10-282-122A-55841
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Score	1824	1689	1292	1274	1268	1268	1268	1265	1264	1261	1258	1257	1257
Result No	40	mσ	r LO	9	7	80	σ	10	11	12	13	14	15

equence 59586, equence 68814, equence 73233, quence 11186, A equence 58419,		equence 651 equence 630 equence 614 equence 614	Sequence 54319, Sequence 48088, Sequence 5599, A Sequence 11328, A Sequence 58718, Sequence 58718,	Sequence 12347, A Sequence 12794, A Sequence 44227, A Sequence 61288, A Sequence 61243, A Sequence 70722, A Sequence 13642, A Sequence 13646, A
.0-282-122A-5958 .0-282-122A-6881 .0-282-122A-7323 9-815-242-11186 .0-282-122A-5841	10-282-122A-5 10-282-122A-5 10-282-122A-4 10-282-122A-4	0-282-122A-6508 0-282-122A-6513 0-282-122A-6305 0-282-122A-6146 0-282-122A-4708	282-122A-5431 282-122A-4808 335-977-5598 335-977-5598 815-242-11328 282-122A-5871	4 6 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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### ALIGNMENTS

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Sequence 12011, Application US/09815242
Sequence 12011, Application US/09805242
Patent No. US200200505341
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Obleson, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Xu, Howard
ITILE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PLILING DATE: 2000-01-23
PRIOR PELICATION NUMBER: 60/207,931
PRIOR PELICATION NUMBER: 2000-12-26
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRAUESQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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120

300

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APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Ku, H.
APPLICANT: Ku, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
RIOR APPLICATION NUMBER: 60/2019,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
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Pred. No. 6.9e-166;
1; Mismatches 1;
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                                                                                                        TYPE: PRT (CRGANISM: Pseudomonas aeruginosa US-10-282-122A-66653
                    SOFTWARE: Patentin version 3.1 SEQ ID NO 66653 LENGTH: 360
                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.4%;
Matches 358; Conservative
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
NUMBER OF SEQ ID NOS: 78614
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APPLICANT: Adamdlo, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant
APPLICANT: APPLICATION UNBERS: US/10/282,122A
APPLICANT: MINGER: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,939
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,336
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
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                                                           Length 360;
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                                                  Score 1824; DB 9;
Pred. No. 6.9e-166;
1; Mismatches 1;
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                                                     Query Match
Best Local Similarity 99.4%;
Matches 358; Conservative
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
  JS-09-815-242-12011
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, John
APPLICANT: Zyskind, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILLE REFERENCE: ELITPA.032.03
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PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION WUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-26
PRIOR PLING DATE: 2001-22-3
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PARCHIN Version 3.1
LENGTH: 360
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
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PRIOR APPLICATION WINBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                               IYPE: PRT
ORGANISM: Pseudomonas syringae
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US-10-282-122A-77459
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 67901
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90.3%; Pred. No. 5.6e-153;
tive 18; Mismatches 17;
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FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT ALING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PLING DATE: 2000-05-66
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Olsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Yanick, John
APPLICANT: Trawick, John
APPLICANT: Yanamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Pseudomonas putida
US-10-282-122A-67901
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Best Local Similarity 90.3%,
Matches 325; Conservative
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US-10-282-122A-69713
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Best Local Similarity
Matches 237; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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66.9%; Pred. No. 5.2e-115;
iive 51; Mismatches 68;
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 77459
LENGTH: 386
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Publication No. US20040029129A1
GENERAL INFORMATION
APPLICANT: Wang, Liangsu
APPLICANT: Aanudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Obleen, Kari
APPLICANT: Obleen, Kari
APPLICANT: Obleen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
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Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 66.9°
Matches 241; Conservative
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; ORGANISM: Vibrio cholerae
US-10-282-122A-77459
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61 GPOSHLSKKGTPTWGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120
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FILE KEKENCE: ELLIKA 1054A

CURRENT AFREKNCE: ELLIKA 1054A

CURRENT FILING DATE: 2003-02-20

PRIOR PEDICATION NUMBER: 60/191,078

PRIOR PEDICATION NUMBER: 60/201

PRIOR PILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-05-09

PRIOR PELING DATE: 2000-05-09

PRIOR PELING DATE: 2000-05-09

PRIOR PELING DATE: 2000-05-09

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2001-12-16

PRIOR PELING DATE: 2001-02-16

PRIOR PELING DATE: 2001-03-11

PRIOR PELING DATE: 2001-03-16

PRIOR PELING DATE: 2000-03-11

PRIOR PELING DATE: 2000
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APPLICANT: Oblsen, Kari L.
APPLICANT: Cyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for
TITLE OF INVENTION: proliferation of B. coli
FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US/09/741,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.4%; Score 1274; DB 12;
65.8%; Pred. No. 2.7e-113;
iive 57; Mismatches 66;
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Patent No. US2002002718A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Pasteurella multocida
US-10-282-122A-66896
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9

SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10028 LENGTH: 360

; ORGANISM: Escherichia coli US-09-815-242-10028

Page

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61 GPESHFSKRGTPIMGGIMILTAIVISVILWAYPSNPYVWCVLVVLVGYGVIGFVDDYRKY 120
                                                                                                                                                                                                                                                                                                                                                                            121 IEKNSRGLPSRWKYFWOSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIOLGIFFVVLT 180
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                                                                                                                                                                            Query Match 69.0%; Score 1268; DB 9; Length 360; Best Local Similarity 66.4%; Pred. No. 1e-112; Matches 239; Conservative 51; Mismatches 70; Indels
CURRENT FILING DATE: 2000-12-19
PRIOR PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 451
LENGTH: 360
TYPE: RAT
TYPE: RAT
US-09-741-669-451
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US-09-815-142-10028

Sequence 10028, Application US/09815242

Sequence 10028, Application US/09815242

Sequence 10028, Application US/09815242

Sequence 10028, Application US/09815242

SEQUENCE INFORMATION:

APPLICANT: Mall, Daniel

APPLICANT: Zyskind, Judith W. APPLICANT: Wall, Daniel

APPLICANT: Yamanco, Robert T. APPLICANT: Yamanco, Robert T.

APPLICANT: Wall, Daniel

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Droxaryotes

FILE REFERENCE: ELITRA 011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR APPLICATION NUMBER: 00/191,078

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27
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; Sequence 56412, Application US/10282122A
; Publication No. U520040029129A1
; GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Mandone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Admine, Cheryl
APPLICANT: Tawaick, John
APPLICANT: Taranten
APPLICANTEN
APPL
Query Match 69.0%; Score 1268; DB 9; Length 3
Best Local Similarity 66.4%; Pred. No. 1e-112;
Matches 239; Conservative 51; Mismatches 70; Indels
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
Remaining Prior Application data removed - S
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SOFTWARE: 96112
LENGTH: 360
                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-56412
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RESULT 10
US-10-282-122A-77920
; Sequence 77920, Application US/10282122A
; Sequence 77920, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Bamudio, Carlos
; APPLICANT: Bamudio, Carlos
; APPLICANT: Asselbeck, Robert
; APPLICANT: Asselbeck, Robert
; APPLICANT: Tawick, John
; APPLICANT: Tawick, John
; APPLICANT: Tawick, John
; APPLICANT: Tawick, Ohn
; APPLICANT: Yamamoto, Robert
; APPLICANT: Yamamoto, Robert
; APPLICANT: Yamamoto, Robert
; APPLICANT: Tayick, Old
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
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ö 61 GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVLVVTLLFGAIGWVDDYRKV 120 61 GPESHFSKRGTPTMGGLMILFSITISVLAWAXPSNPYVWCVLFILIGYGIVGFIDDYRKV 120 121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180 181 YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 240 241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME 300 301 TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR 360 9 1 MILLLABYLQOFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND Gaps ö Query Match

68.9%; Score 1265; DB 12; Length 360;
Best Local Similarity 65.6%; Pred. No. 2e-112;
Matches 236; Conservative 54; Mismatches 70; Indels 0 PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - 6
SCHWARE: Patentin Version 3.1
SEQ ID NO 77920
LENGTH: 360 ; TYPE: PRT ; ORGANISM: Yersinia pestis US-10-282-122A-77920

APPLICANT: GNBELLOCK, KALL
APPLICANT: Cylsen, Valid
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITAR.034
TILLE OF INVENTION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23 Sequence 76018, Application US/10282122A
Publication No. US20040029129A1
PUBLICANT: NEORATION:
APPLICANT: Mang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hagelbeck, Robert US-10-282-122A-76018 APPLICANT: APPLICANT: APPLICANT:

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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-29
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
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PRIOR DA
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08-10-282-122A-75186
US-10-282-122A-75186
Squance 75186, Application US/10282122A
Squance 75186, Application US/10282122A
Squance 75186, Application No. US20040029129A1
Squance 75187 Nang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Assolbeck, Robert
APPLICANT: ApplicANT: ApplicANT: Ohlsen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
APPLICANT: Yamanoto, Robert
APPLICANT: Forsyth, R.
ITILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
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PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-08
PRIOR PILING DATE: 2001-02-08
PRIOR PILING DATE: 2001-02-08
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-08
PRIOR PILING DA
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61 GPOSHLSKKGTPIMGGALILIFALALSTLLWADLSNRYVWVLVVTLLFGALGWVDDYRKV 120

61 GPESHFSKRGTPTMGGIMILTSIVISVLAMAYPSNPYVWCVLVVLIGYGIIGFVDDYRKV

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Query Match 68.6%; Score 1261; DB 12; Length 360; Best Local Similarity 65.8%; Fred. No. 4.7e-112; Matches 237; Conservative 53; Mismatches 70; Indels 0

121 IEKNSRGIPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180

181 YFVIVGSSNAVNITDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 240 

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Sequence 14075, Application US/09815242;
Patent No. US2002061569A1;
REPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari L.;
APPLICANT: Zyskind, Judith W.;
APPLICANT: Trawick, John D.;
APPLICANT: Trawick, John D.;
APPLICANT: Carr, Grant J.;
APPLICANT: Trawick, John D.;
APPLICANT: Yamamoto, Robert T.;
APPLICANT: Yumamoto, Robert T.;
APPLICANT: Xu, H. Howard
                                                                                                         RESULT 13
US-09-815-242-14075
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301 ILSVMIQVASFKLTGRRVFRMAPIHHHPBLKGWPDPRVIVRFWIITVILVLIGLATLKTR 360

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301 TLSVMIQVASFKLIGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 IVCTAIVGAGLGFLWFNIYPAQVFMGDVGSLALGGALGIIAVLLRQEFLLVIMGGVFVVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 360
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE OF INVENTION: Prokaryotes FILE OF INVENTION: Prokaryotes CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-05-32 PRIOR FILING DATE: 2000-05-32 PRIOR FILING DATE: 2000-05-36 PRIOR APPLICATION NUMBER: 60/242,578 PRIOR FILING DATE: 2000-10-33 PRIOR PLING DATE: 2000-10-37 PRIOR PRIOR DATE: 2000-10-37 PRIOR PLING DATE: 2000-10-37 PRIOR PRIOR DATE: 2000-10-37 PRIOR PLING DATE: 2001-10-37 PRIOR PLING DATE: 2001-10-37 PRIOR PLING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR PLING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 14110 SEQ ID NO 11691 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: 2001-02-16 NUMBER OF SEQ ID NO 11691 PRIOR DATE: 2001-02-16 NUMBER OF SEQ ID NO 11691 PRIOR PRI
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Best Local Similarity 65.6%; Pred. No. 1.1e-111;
Matches 236; Conservative 52; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-010-282-122A-55841
Sequence 55841, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICAMT: Wang, Liangeu
APPLICAMT: Haselbeck, Robert
APPLICAMT: Haselbeck, Robert
APPLICAMT: Zyskind, Judith
APPLICAMT: Zyskind, Judith
APPLICAMT: Wall, Daniel
APPLICAMT: Trawick, John
APPLICAMT: Trawick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-815-242-11691
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65.8%; Pred. No. 9.2e-112;
iive 52; Mismatches 71;
                                             Essential
                         TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR PRILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SECIENTIAN SECIENTIAN
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Sequence 11691, Application US/09815242
Sequence 11691, Application US/09815242
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Karl L.
APPLICANT: Ollsen, Karl L.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
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COCATTON: (1)...(360)
COTHER INFORMATION: Xaa = Any Amino Acid
NS-09-815-242-14075
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Best Local Similarity 65.81
Matches 237; Conservative
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILS REFERENCE: ELITRA,034
CURRENT APPLICATION NUMBER: 02/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/20/127
PRIOR PELICATION NUMBER: 60/20/727
PRIOR APPLICATION NUMBER: 60/20/30/335
PRIOR APPLICATION NUMBER: 60/20/30/347
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230/347
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/25/,625
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-55841
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                                                                            May 7, 2004, 08:37:38 ; Search time 23 Seconds (without alignments) 808.059 Million cell updates/sec
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1837
1 MLLLLAEYLQOFYKGFGVFQ......RFWIITVILVLIGLATLKLR 360
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-09-512-522-525-525-525-525-525-525-525-525	INO ACID SEQUENCES RELATING NOSTICS AND THERAPEUTICS 1A	; DB 4; Length 467; 2.2e-197; tes 1; Indels 0; Gaps .TALSLSLWLGPWMIRTLQIPQIGQAVRND			EKNSRGLPSRWKYPWQSVPGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 
		DB 4; 1 2.2e-197; 1es 1; TALSISLWIC	  ALSLSLWLC  LSNRYYWV	  SNRYVWV	PIETTL
,66666666666666	SULT 1 -09-22-991A-24194 Sequence 24104, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 LENGTH: 467 TYPE: PRI CRGANISM: Pseeudomonas aeruginosa	99.3%; Score 1824; DB imilarity 99.4%; Pred. No. 2.2e-1 ; Conservative 1; Mismatches MLLLLAEYLQQPYKGFGVPQYLTLRGILSVLTALSL			VFGIGAAVFLYMTAE:                  VFGIGAAVFLYMTAE:
. 4 8 8 9 1 8 4 8 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	pplication US/09 N: N: A: N:	99.3%; 99.4%; ative	OPYKGFGV STPTMGGAL	TPTMGGAL	SRWKYFWQS          SRWKYFWQS
, www.uww.oooooow.uww.uww.uw.u	ULT 1  99-252-991A-24194  atent No. 6551795  ENERAL INNOFAMATION: TITLE OF INVENTION: NUCLEIC ACID AN TITLE OF INVENTION: NUCLEIC ACID AN TITLE OF INVENTION: AERUGINOSA FOR FILE REFERENCE: 107196-136 CURRENT APPLICATION NUMBER: US/09/25 CURRENT FILING DATE: 1999-02-18 PRIOR PILLING DATE: 1999-02-18 PRIOR FILLING DATE: 1998-02-18 PRIOR FILLING DATE: 1998-07-27 WUMBER OF SEQ ID NOS: 33142 LENGTH: 467 TYPE: PRT ORGANISM: PSeudomonas aeruginosa 09-252-991A-24194	h Similarity 99. 58; Conservative MILLIARYLOOFYKG	LLLLAEYLÇ	<u>—</u> გ	⊠¤
11111111111111111111111111111111111111	ESULT 1  18-09-252-991A-24194  Patent No. 6551795  GENERAL INFORMATION:  APPLICANT: MARC J.  TITLE OF INVENTION:  TITLE OF INVENTION:  CURRENT APPLICATION INTO THE REFERENCE:  CURRENT FILING DATE:  PRIOR PILING DATE:  PRIOR PLING DATE:  NUMBER OF SEQ ID NOS  SEQ ID NO 24194  LENGTH: 467  LENGTH: 467  LYPE: PRI  CRGANISM: Pseudomon.  IS-09-252-991A-24194	Query Match Best Local Si Matches 358;	108 M		121 I 228 I
1 (G W W W W W W W W A A A A A A 0 (C W W W W W W W W A A A A A A	RESULT 1 US-09-252 Sequence   Patent   GENERAL   FITTLE   TITLE   TITL	Quer Best Matc	රි සි	7 원	දු පු

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347 300

Y FVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI

360 467

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US-09-489-039A-12439

Sequence 12439, Application US/09489039A

Sequence 12439, Application US/09489039A

Sequence 12439, Application US/09489039A

Sequence 12439, Application US/09489039A

Sequence 12439, Application US-09489039A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US-09489,039A

CURRENT APPLICATION NUMBER: US-09/489,039A

CURRENT ELLING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US-06/117,747

NUMBER OF SEQ. ID NOS: 14342

SEQ. ID NO 12439
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                                                                            61 APENHAKKOGTPTMGGILILLSIGISTLLWADLSNPYVWIVLGVWVVFGAVGWADDWIKI 120
                                                                                                                                 121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYM--TAETPIETT-----LIVPMLKSVBI--- 170
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196 YFVIVGTGNAVNLTDGLDGLAIMPTVFVAAGFALVAWATGNWNFANYLHIPYLRHAGELV
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                                                          61 GPOSHLSKKGTPIMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12439
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361 LVVLGLMTLKLR 372
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                                     Sequence 6169, Application US/09328352
Pacent No. 6562958
Patent No. 6562958
TERMINED INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION SAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF ILING DATE: 1099-06-04
CURRENT FILING DATE: 1099-06-04
SEQ ID NO 6169
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Best Local Similarity 65.0%; Pred. No. 1.1e-132;
Matches 234; Conservative 56; Mismatches 70; Indels
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Best Local Similarity 58.6%; Pred. No. 9.9e-118;
Matches 218; Conservative 62; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
US-09-328-352-6169
                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Prote
US-09-543-681A-705;
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MLLLLAEYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND

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RESULT 7
US-09-107-532A-5276
US-09-107-532A-5276
Sequence 5276, Application US/09107532A
Sequence 5276, Application US/09107532A
Sequence 5276
BATEL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
SETTLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                              88 ILWADLSNRYVWVVLVVTLLFGAIGWVDDYRKVIBKNSRGLPSRWKYFWQSVFGIGAAVF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                         264 FMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVMETLSVMIQVASFKLIGRRVFRMAP 323
                                                                                                                 135 FFVLSDVFHLVHFTTDLHIPFV-NFDIPLSFAXVIFIVFWQVGFSNAVNLTDGLDGLAT-
                                                                                                                                                                                                                                                                                                                                                                               80 IIFVDHSNPII-LLLFVTIGFGLIGFIDDYIIVVKKNNQGLTSKQKFLAQIII----AVI
                                                                                                                                                                                                                                                               LYMTAE----TPIETTLIVPMLKSVEIQLGIFFVVLTYFVIVGSSNAVNLTDGLDGLAIM
                                                                                                                                                                                                                                                                                                                                                     204 PTVMVAGALGIFCYLSGNVKFAEYLLIPNVFGAGELIVFCAALVGAGLGFLWFNTYPAQV
                                                                                          31 LTALSLSLWLGPWMIRTLQIPQIGQAVRNDGPQSHLSKKGTPTWGGALILTAIAIST---
                                              Gaps
                                                28;
  Length 334;
                                              93; Indels
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CORRESPEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
34.6%; Score 636; DB 4;
42.3%; Pred. No. 2.5e-63;
tive 70; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISOS660
COMPUTER: PC
OPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 IHHHFELSGWGEWKVVTVFWTVGLITGLIGL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 IHHHFELKGWPDPRVIVRFWIITVILVLIGL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 331 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5276:
SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
    Query Match
Best Local Similarity 42.39
Matches 140; Conservative
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                                                                                                        US-09-540-236-3138
Sequence 3138, Application US/09540236
Facent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NOS: 3840
SEQ ID NOS: 3840
SEQ ID NOS: 3840
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: PUDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION WUMBER: US/09/134,001C
CURRENT FILING DATE: 1999-08-13
PRIOR PELICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKVIEKNSRGLPSRWKYFWQSVFG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 LGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVMETLSVMIQVAS 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 LGFLWYNAAPADVFMGDVGALSLGGMLGTIAVMTRQELAFAIMGGIFVAEAVSVILQVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 LTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRNDGPQSHLSKKGTPTMGGALILT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 IGAAVFLYMTAETPIETTLI-----VPMLKSV-----EIQLGIFFVVLTYFVIVGSSNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.8%; Score 970.5; DB 4; Best Local Similarity 52.6%; Pred. No. 4.6e-101; Matches 184; Conservative 69; Mismatches 86;
  ||||::|| ||||
TLSVILQVGSFKLR----RSAHLPH 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3851, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ), ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3851
                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: M.catarrhalis
US-09-540-236-3138
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US-09-134-001C-3851
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HHHFELKGWPDPRVIVRFWIITVI 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 GLATLKLR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 GIAAVLWR 349
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US-08-986-768-2
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Patent No. 6617156

GENERAL INCOMPATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERBNCE: 032796-032

CURRENT ELING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 LAMGLFFHQFTPSLLIILFILVLYGLLGYLDDFIKVFKKRNMGLNSRQKLIGQ-IF--GG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLWADLSNRY---VWVVLVVTLLFGAIGWVDDYRKVIEKNSRGLPSRWKYFWQSVFGIGA 144
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                                                                                                                                                                                                                                                                                                                                                         DGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELIVFCAALVGAGLGFLWFN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                       140 FGIGAAVF--LYMTAETPIETTLIVPMLKSVBIQLGIFFVVLTYFVIVGSSNAVNLTDGL 197
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                                                                                                                                                                                                                                                                                                                 GGI---IFYLVYRSEGYPGVLNFF----GLDLPLGIIYGIFALFWLVGFSNAVNLTDGI
                                                                                                                                                                                                                               LTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKVIEKNSRGLPSRWKYFWQSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 LSVLTALSLSLWLGPWMIRTLQIPQIGQAVRNDGPQSHLSKKGTPTMGGALILTALAIST
                                                                                                                                                                                                   16 QALIPIVSSCAMTIAAMPLFIGYFQMKKQGQAIREEGPKWHNSKAGTPTMGGLVFLIGSI
                                                                                                                                                                     25 RGILSVLTALSLSLBLWGPWMIRTLQIPQIGQAVRNDGPQSHLSKKGTPTMGGAL----I
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                                                                                                                                      32;
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                                                                                                      Length 331,
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                                                                                                     32.3%; Score 593; DB 4; Length 33 38.0%; Pred. No. 1.8e-58; tive 75; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 VFRMAPIHHHPELKGWPDPRVIVRFWIITVILVLIGL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.8%; Score 583.5; DB 4; Best Local Similarity 38.6%; Pred. No. 2.1e-57; Matches 125; Conservative 68; Mismatches 108;
                NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...331

SEQUENCE DESCRIPTION: SEQ ID NO: 5276:
US-09-107-532A-5276
Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis
                                                                                                                       Local Similarity 38.09
nes 128; Conservative
 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-134-000C-4685
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              FEATURE
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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Sequence 973, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICATION:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering RIPLE OF INVENTION: and treatment of infection
FILE REPERSING: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 VPGAGELIVFCAALVGAGLGFLWFWTYPAQVFWGDVGALALGAALGTIAVIVRQEIVLFI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 LEMLHKDKAEVPTGGGVLLFISLIASLLVWLPWGKFSTWFFILLTCYAGLGWYDDRIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 KRKQGHGLKAKHKEMVQIAIAAPTLIALPYIYGSTE-PL-WTLKIPFMEGMLSLPFWLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 TVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELIVFCAALVGAGLGFLWFNTYPAQVF
                         MGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVMETLSVMIQVASFKLTGRRVFRMAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MILLLABYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 MGGVFVMETLSVMIQVASFKLIGRRVFRMAPIHHHFBLKGWPDPRVIVRFWIITVILVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosteck Jr, Paul R
TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: MraY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 29.7%; Score 546.5; DB 4; Length Best Local Similarity 35.1%; Pred. No. 3.5e-53; Matches 129; Conservative 75; Mismatches 137; Indels
```

```
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 LIGRRVFRMAP---IHHHFELKGWPDPRVIVRFW--
                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECHMUNICATION INFORMATION:
TELEPHONE: (781)893-8077
ITELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4764:
SEQUENCE CHARACTELISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...386

SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

US-09-107-532A-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                        COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LIGLATLK 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 AMLFAAILLFELİĞLINEK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 386 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                         ZIP: 02354
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-634-238-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette Acid AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 LLGGV--IFYLFYERGGDLLSVFGYP-----VHLGFFYIFFALFWLVGFSNAVNLTDGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 HKPAKVFWGDVGSLALGGMLAAISMALHQEWTLLIGIVYVFETTSVMMQVSYFKLTGGK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TAIAISTLLWADLSNRY---VWVVLVVTLLFGAIGWVDDYRKVIEKNSRGLPSRWKYFWQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 SVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLTYFVIVGSSNAVNLTDGL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 TYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVMETLSVMIQVASFKLT-GR 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 LTLVGI------PAFIQFYRKAQITGQQMHEDVKQ-HQAKAGTPTMGGLVFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 DGLAIMPTVMVAGALGIFCYLSGNVKFABYLLIPNVPGAGELIVFCAALVGAGLGFLWFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 ITLRGILSVLTALSLSLWLGPWMIRTLQIPQI-GQAVRNDGPQSHLSKKGTPTWGGALIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 RVFRMAPIHHHFELKG-----WPDPRVIVRFWIITVILVLIGLATLKL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 RIFRMTPVHHHFELGGLSGKGNPWSEWKVDFFFWGVGLLASLLTLALLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.3%; Score 520; DB 3; Length 32 36.9%; Pred. No. 3.1e-50; Artive 60; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,768
FILING DATE: December 8, 1997
CLASSIFICATION: 424
                                       ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTATION UNMER: 39,872
REFERENCE/DOCKET NUMBER: X-117
REFERENCE/DOCKET NUMBER: X-117
REPERDOM/UNICATION INFORMATION:
TELEPHONE: 317/276-3334
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 326 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-986-768-2
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                        STATE: Indiana
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-107-532A-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 129
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139 VFGIGAAVELYMTAETPIETTLIVPMLKSVEIQLGIFFVVLTYFVIVGSSNAVNLTDGLD 198 199 GLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELIVFCAALVGAGLGFLWFNT 258 .---- 350 259 YPAQVEMGDVGALALGAALGTIA-----VIVRQEIVLFIMGGVFVMETLSVMIQVASFK 312 275 KANRVSFSTADKKHLHHRLISLGFTHKGAVLTIYAMALMFSFTAMVMVTGRİGİLİLII 334 66 ISFVIŠTLFLFRKIIPQSYIVPILIASLVIIVTGVLDDKYELTPKQ-------KS 22 LTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRNDGP-OSHLSKKGTPTMGGALIL 81 TAIAISTILM--ADLSNRYVWVVLVVTLIFGAIGWVDDYRKVIEKNSRGLPSRWKYFWQS Gaps 82; Length 386; Indels Query Match
13.3%; Score 245; DB 4; L
Best Local Similarity 26.6%; Pred. No. 4.9e-19;
Matches 101; Conservative 65; Mismatches 131;

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Sequence 92, Application US/08846762A;
Sequence 92, Application US/08846762A;
Batent No. 5994072
GENERAL INFORMATION:
APPLICANT: Law, Joseph S.
APPLICANT: Charter, Deborah
APPLICANT: Charter, Deborah
APPLICANT: Charter, Teresa
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
TITLE OF INVENTION WUMBER: US/08/946,762A
CURRENT APPLICATION WUMBER: US/08/946,762A
CURRENT PILING DATE: 1997-04-30
SOFTWARE: PATENTION OF O-ANTIGEN OF SEQ ID NO 92
LENGTH: 341
TYPE: PRT
CREATER PRT PREMAMER: Pseudomonas aeruginosa
US-08-646-762-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1245, Application US/09489039A

Patent No. 6610886

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 1000-01-27
PRIOR PLLING DATE: 1099-01-29
NUMBER OF SEQ ID NOS: 14342

LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                      291 -----FIMGGVFVMETLSVMIQVASFKLTGRRVFR--MAPIHHHFELKGWPDPRVIVRFW 343
                                                                                                                                                                                                                                                                                                                                              118 RKVIEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAET-----PIETTLIVPMLKSVEIQ 171
                                                                                                        172 LGIFFVVLTYFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIP
                                                                                                                                 309 ASFKLIGRRVFRMAPIHHHPELKGWPDPRVIVRFWIITVILVLIGLATLKLR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 APLSCAGQRIFRMAPIHHYELKGWPEFRVIVRFWIISLMLVLIGLATLKVR 69
                                                 112 LKLAGO------IVAALIVTFYGITIDFISLPIGPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.1%; Score 222; DB 4; Length 69
Best Local Similarity 75.0%; Pred. No. 1.5e-17;
Matches 39; Conservative 8; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-12452
                                                                                                                                                                                                                                                                                                                                                                                                                           344 IITVILVL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 SIAIMFSL 313
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US-09-489-039A-12452
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: E910670134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PRILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674

LENGTH. 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 KPISVMGGTVILFSFLIGIWLGHPIERE------VKPLILGAITMYMVGLIDDIYDLRPY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 TLIVPMIKSVEIQLGIFFVVLTYFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 SGNVKFAEYLLIPNVPGAGELIVFCAALVGAGLGFLWFNTYPAQVFWGDVGALALGAALG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TLWVPVLGNVNATW--FYVIFVVFWLVGFSNAVNLTDGLDGL------VAG----- 43
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                                                                             APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, Ilkka J.
APPLICANT: Blobese, Leonard, N.
APPLICANT: Blobese, Leonard, N.
APPLICANT: Blobese, Mark W.
APPLICANT: Chistensson, Anna C.
APPLICANT: Chistensson, Anna C.
APPLICANT: O'TOOle, Paul W.
APPLICANT: O'TOOle, Paul W.
APPLICANT: O'TOOle, Paul W.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, consignition:
FILE REFERENCE: 11000104301
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT PILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARET FASTESED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
12.6%; Score 231.5; DB 4; Length 106;
Best Local Similarity 45.5%; Pred. No. 2.3e-18;
Matches 56; Conservative 14; Mismatches 36; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Staphylococcus epidermidis
        Sequence 311, Application US/09634238
Patent No. 6544772
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 TIA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 VAA 106
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US-09-134-001C-5489
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Best Local Similarity 24.7%; Pred. No. 4e-13; Matches 83; Conservative 57; Mismatches 116; Indels 80; Gaps 16;	FQYLTLRGILSVLTALSLSLSLWLGPWMIRTLQIPQIGQAVRNDGPQSHLSK-KGTPTM 74	FFLLTIFFLLSVGLTYLLIRLXALKONIIDTPNSRSSHVTPTRG 48	75 GGALILTAIAISTLIMADLSNRYVWVVLVVTLLFGAIGWVDDYRKVIEKNSRGLP 129	GGVAIVISFLIGIILFYFLGYLPILSVVGLIVSGGVIALVGFWDDHGHIAAR 100	SRWKYFWQSVFGIGAAVF-LYMTAETPIETTLIVPMLKSVBIQLGIFFVVLIYFVIVGSS 188		NAVNITDGLDGLAIMPTVMVA-GALGIFCYLSG-NVKFAEYLLIPNVPGAGELIVFCAAL 246		GAALGTIAVIVRQEIVLFIMG		LSVMIQVASFKLTGRRVFRMAPI 324	TWTLVRRVLGGFKVYEAHRSHGYQIASRRFKRHLPV 290
Similarity 24.7% 83; Conservative	FOYLTLRGILSVLTALS	FFLLTIFFLLSVGLTYL	GGALILTAIAISTLLWA	GGVAIVISFLIGIILFY	SRWKYFWQSVFGIGAAV	WRLLAHFSAAA)	NAVNLTDGLDGLAIMPT		VGAGLGFLWFNTYPAOV			
ocal S	19	ιΩ	75	49	130	101	189	149	247	199	302	255
Best Loc Matches	δλ	qa	ò	οgα	٥'n	qq	δ	qq	ò	qq	δ	qū

Search completed: May 7, 2004, 08:41:31 Job time: 24 secs

May 7, 2004, 08:37:37 ; Search time 59 Seconds (without alignments) 1724.019 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. using sw model - protein search, OM protein Run on:

US-10-089-787-2 1837 1 Milllaeylqqeykgfgvfq......RWIITVILVLJGLATLKLR 360 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp2000s:\*

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SUMMARIES	ΩI	AAB73487	AAU36418	ABU38729	ABU39977	ABU41789	ABU49535	ABM68871	ABU38972	AAU34435	AAG98403	ABU28488	ABU49996	ABU48094	ABU47262	AAU38482	AAU36098	ABU27917	ABU31662	ABU40890	ABU45309	AAU35593	ABU30495	ABU22089	ABU23453	ABU21181
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## ALIGNMENTS

AAB73487 standard; protein; 360 AA. RESULT 1

AAB73487;

17-JUL-2001 (first entry)

Pseudomonas aeruginosa MraY protein.

MraY; phospho-N-acetylmuramoyl-pentapeptide translocase; peptidoglycan biosynthesis; bacterial cell wall; infection; drug screening; antibacterial; Pseudomonad; G+C rich bacterium.

Pseudomonas aeruginosa

WOZ00125251-A1.

12-APR-2001.

29-SEP-2000; 2000WO-US027056.

04-OCT-1999; 99US-0157580P.

(MERI ) MERCK & CO INC

El-Sherbeini M, Azzolina B;

WPI; 2001-308221/32. N-PSDB; AAF86639.

New MraY gene and enzyme of Pseudomonas aeruginosa, useful in vitro assays for screening antibacterial compounds that target cell wall biosynthesis, particularly for screening antibiotics against Pseudomonads.

Claim 15; Fig 1; 22pp; English.

This sequence represents the Pseudomonas aeruginosa phospho-N-acetylmuramoyl-pentapeptide translocase, designated MraY. The MraY protein is involved in bacterial cell wall biosynthesis. It catalyses the first step of the membrane cycle of peptidoglycan biosynthesis, i.e., the transfer of an N-acetylmuramic acid peptido lyon a bactoprenol phosphate carrier molecule. The MraY protein is useful in in vitro assays to screen for antiparterial compounds that target cell wall biosynthesis. Inhibitors of the MraY protein are useful in preventing the growth of Pseudomonads and other G+C rich bacteria. Pseudomonas aeruginosa is an opportunistic pathogen which causes infections in patients with burns, 

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neutropenia, or cystic fibrosis. Primers or probes derived from the mray gene are useful in nucleic acid amplification-based assays for detecting the presence of a polynucleotide encoding Pseudomonas aeruginosa Mray
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23-MAY-2000; 2000US-0206848P.
23-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0258655P.
25-DEC-2000; 2000US-0258658P.
16-FEB-2001; 2001US-0259308P.
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antibacterial; drug design.
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N-PSDB; AAS54277.
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99.3%; Score 1824; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 6.1e-192;
Matches 358; Conservative 1; Mismatches 1; Indels C
New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #24256
                        Example 3; SEQ ID NO 12011; 511pp; English.
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The invention relates to an isolated mucleic acid comprising any one of the invention relates to an isolated mucleic acid inhibited by the antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated contained by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contributes the proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for challed for proliferation, or that inhibits callular proliferation; (8) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acter, (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture comprising strains in which the gene or organism. The artiture of an organism. The artiture of a compound that inhibits the proliferation of an organism. The artiture of a compound that inhibits the compound and proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for molecules for rational confidence or proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not format directly from WIPO at the print proliferation for the print proliferation and profilerati New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. Claim 25; SEQ ID NO 66653; 1766pp; English. 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-CCT-2001; 2001US-034292BP. 08-FEB-2002; 2002US-0362859P. 21-MAR-2002; 2002WO-US009107 (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, WPI; 2003-029926/02. N-PSDB; ACA42599. 'n, Wang Wall 

Sequence 360 AA

120 61 GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120 121 IBKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180 9 9 1 MLLLLAEYLQQFYKGFGVFQYLTLRGILLSVLTALSLSLWLGFWMIRTLQIRQIGQAVRND 61 GPQSHLSKKGTPTMGGALILTAIAISTLLMADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 1 MLLLLAEYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND Gaps .; 0 Score 1824; DB 6; Length 360; Pred. No. 6.1e-192; 1; Mismatches 1; Indels ( 99.3%; Matches 358; Conservative Query Match Best Local Similarity g ò 셤 ò 용

YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 240

360 360 241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME 301 TLSVMIQVASFKIJGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR 241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME g g g ઠે

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

ABU39977 standard; protein; 360 AA

ABU39977;

(first entry) 19-JUN-2003 Protein encoded by Prokaryotic essential gene #25504

Antisense; prokaryotic essential gene; cell proliferation; drug design

Pseudomonas putida

WO200277183-A2.

03-OCT-2002

21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00372851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Š Zyskind . Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, Wang L, Wall D,

WPI; 2003-029926/02. N-PSDB; ACA43847.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 67901; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the RESULT 4

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New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for callular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

8X888888888X8

Sequence 360 AA;

Claim 25;

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid containing the vector; (3) an isolated encoding a polypeptide whose expression is inhibited by the antisense conclined to its fragment whose expression is inhibited by the antisense conclined or its fragment whose expression is inhibited by the antisense conclined to its fragment whose expression is inhibited by the prolypeptide or its fragment whose expression is inhibited by the antisense the activity of antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or that has an activity against a biological pathway broliferation, or that has an activity against a biological pathway required for that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound sactivity; (1) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which confideration of an organism. The antisense nucleic acids required for callular proliferation to isolate and antisense callular acids are useful for termination or proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this proliferation format directly from WIPO at sequences 

Sequence 360 AA;

180 180 240 61 GPQSHLSKSGTPTMGGALILSSIGISTLLWADLSNRYVWVLLVTFLFGAIGWVDDYRKV 120 300 9 121 IEKNSRGLPSRWKYFWQSVFGLCAAIFLYTTAPSATETTLIVFWLKDVRIPLGIGFIVLT 121 JEKNSRGLPSRWKYFWGSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME MLLLLAEYLQQFYKGFGVFQYLTLRGILSVLTALSISLWLGPWMIRTLQIPQIGQAVRND 301 TLSVMIQVASFKLTGRRVFRMAPIHHHPELKGWPDPRVIVRFWIITVILVLIGLATLKLR GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV Gaps .; 0 Query Match 90.3%; Score 1658; DB 6; Length 360; Best Local Similarity 89.7%; Pred. No. 1.2e-173; Matches 323; Conservative 17; Mismatches 20; Indels C Н 61 Query Match Best Local S a g 셤 δ 원 8 ò 8 ઠે

ö 181 YFVIVGSSNAVNLTDGLDGLAIMPTVWVGGALGIFCYLSGNVKFAEYLLIPYVFGSGELI 240 GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVIVVTLLFGAIGWVDDYRKV 120 GPQSHLSKSGTPTWGGALILSAIAVSTLLWADLSNRYVWVVLIVTLAFGAIGWVDDYRKV 120 | IEKNRRGLPRRWKYFWQSVFQIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180 YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 240 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME 300 9 90 1 MILILAEYLQQPHKGFAVPQYLSIRGILGVLTALSLALWIGPWMIRTLQIRQIQQAVRND 1 MILLIAEYLQQFYKGFGVPQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND Gaps . 0 Length 360; 91.9%; Score 1689; DB 6; Length 3 90.3%; Pred. No. 4.6e-177; cive 18; Mismatches 17; Indels Query Match Best Local Similarity 90.3° Matches 325; Conservative 61 121 241 301 181 8 6 8 6 8 d ò  $\dot{\circ}$ 음상

Antisense; prokaryotic essential gene; cell proliferation; drug design encoded by Prokaryotic essential gene #27316. ABU41789 standard; protein; 360 21-MAR-2002; 2002WO-US009107 (first entry) Pseudomonas syringae WO200277183-A2. 19-JUN-2003 03-OCT-2002 ABU41789 Protein 

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-0362699P. ELITRA PHARM (ELIT-)

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, 'nά Wang |

screening SEQ ID NO 69713; 1766pp; English.

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ABU49535 standard; protein; 360 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-03072851. 06-MAR-2002; 2002US-0362699P. ABU49535; Wang I Wall I ABU49535

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Antisense; prokaryotic essential gene; cell proliferation; drug design Protein encoded by Prokaryotic essential gene #35062 21-MAR-2002; 2002WO-US009107 (first entry) Vibrio cholerae. WO200277183-A2 03-OCT-2002

(ELIT-) ELITRA PHARM INC.

Zyskind JW; Xu HH; Haselbeck R, Ohlsen KL, Yamamoto R, Forsyth RA, Malone C, Carr GJ, Zamudio C, Trawick JD, , c,

WPI; 2003-029926/02. N-PSDB; ACA53405.

screening 1 to New antisense nucleic acids, useful for identifying proteins or e for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 77459; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid chidibites proliferation of the nucleic acid (1) a nost cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense collypeptide or its fragment whose expression is inhibited by the antisense proliferation or the activity of apply peptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway to required for proliferation, or that inhibits cellular proliferation; (6) identifying a compound that inhibits on the biological pathway in which a proliferation or required for cellular proliferation or the biological pathway in which a proliferation required for cellular proliferation of an organism acts; (9) manifacturing an antibiotic; (10) profiling a compound; sactivity; (11) a culture comprising strains in which the gene or which each of the strains is present in a culture or collection of an organism. The antisense nucleic acids are useful for the proliferation of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhmurium, C. the target prokaryotic essential genes note: The sequence data for this conficulation but was obtained the larget prokaryotic essential genes. Note: The sequence data for this conficulation, but was obtained for proliferation in cells other than S. aureus, S. typhmurium of the printed for proliferation in cells other than S. aureus, S. typhmurium of the printed specification, but was obtained for proliferation of the printed specification, but was obtained for in electronic format directly from Willey and the sequences.

Sequence 360

ö 301 TLSYMIQVASFYLTGERVPRNAPIHHHPELKGWPDPRVIVRFWIITVILVLIGLATLKUR 360 301 TLSVILQVGSYKLRGQRIFRMAPIHHHYELKGWPEPRVIVRFWIISIVLVLJGLATLKVR 360 120 180 240 240 300 1 MILLILABYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND 60 9 Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; whooping cough. 61 GPESHFSKRGTPIMGGVMILAAITITVLLMADLTNPYVMAVLAVLLGYGAVGFVDDYRKV 241 VFCAALVGAGLGFLWFNIYPAQVFWGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVWE
241 VVCTAMVGAGLGFLWFNIYPAQVFMGDVGALALGGALGTIAVLVRQEFVLVIMGGVFVWE GPQSHLSKKGTPIMGGALILIAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 181 YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI Gaps .. 0 Length 360; Indels cch 70.3%; Score 1292; DB 6; al Similarity 66.9%; Pred. No. 2.6e-133; 241; Conservative 51; Mismatches 68; Photorhabdus luminescens protein sequence #1968. ABM68871 standard; protein; 361 AA. (first entry) 20-NOV-2003 Query Match Best Local Si Matches 241, 61 ABM68871; RESULT 7 ABM68871 ò 셤 g 셤 8 8 8 ò

EL, Glaser P, Frangeul L, Kunst RECH SCI 07-FEB-2002; 2002WO-IB003040 07-FEB-2001; 2001FR-00001659 Photorhabdus luminescens. Taourit S, (INSP ) INST PASTEUR. (CNRS ) CNRS CENT NAT 40200294867-A2 28-NOV-2002 

Danchin A; WPI; 2003-148459/14. Duchaud E, Ta Buchrieser C;

Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides Claim 2; SEQ ID NO 1968; 1205pp; French

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms, for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms for detection/identification

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Zyskind Xu HH;

ELITRA PHARM INC.

(ELIT-)

us-10-089-787-2.rag

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carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, response or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens are useful for recombinant production of the protests the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The antibacterials useful as insecticides, bactericides and fungicides. The cancel proteins, vectors containing the genes and Ab are also useful the are sensitive to P. luminescens and the proteins are as virulence is escentified. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
              $5555555555555555888
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Sequence 361 AA;

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240
                                                                                                                                                                                                                                                                            GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120
                                                                                                        IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180
                                                                                                                                                                 180
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                                                                                                                                                                                                                                               9
                                                               1 MLVWLAEYLVKYHSGFNVFSYLTFRAIVSLLTALAIALWMGPRMIAFIQKLQIGQVVRND 60
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VRKDIKGLIARWKYFWQSVLALGVAFAMYSFGKDTPATQLVVPFFKDVMPQLGVLYILLT
                                                                                                                                                                                       YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI
                                                1 MULLLABYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND
                          Gaps
                          ·.
    Length 361;
                          Indels
                          99
  69.7%; Score 1280; DB 6;
66.4%; Pred. No. 5.5e-132;
iive 55; Mismatches 66;
                          Conservative
Query Match
Best Local Similarity
Matches 239; Conserv
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Antisense; prokaryotic essential gene; cell proliferation; drug design. gene #24499 essential ABU38972 standard; protein; 360 encoded by Prokaryotic 2001US-00815242. 2001US-00948993. 2001US-0342923P. 2002US-00072851. 2002US-0362699P. 2002WO-US009107 (first entry) Pasteurella multocida WO200277183-A2. 21-MAR-2001; 2 06-SEP-2001; 2 25-OCT-2001; 2 08-FEB-2002; 2 06-MAR-2002; 2 21-MAR-2002; 19-JUN-2003 03-OCT-2002 ABU38972 Protein RESULT 8

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concluded are:

(2) a vector comprising a promoter operably linked to the nucleic acid.

(3) an isolated concluding the polypeptide of specifically binding the polypeptide of the activity of antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or that has an activity against information; (8) required for proliferation, or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway required for proliferation or that the activity against a biological pathway required for proliferation or the test compound that inhibits proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for molecules for callular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for proversed or called for form part of the printed for term part of the printed 
                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                           ąğ
                                           Ohlsen |
Forsyth |
                                           Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                   66896; 1766pp; English.
                                           Malone C,
Carr GJ,
                                           Zamudio C,
Trawick JD,
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                                                                                                                2003-029926/02
                                                                                                                                                                                                                                                                                   25; SEQ ID
                                                                                                                                       N-PSDB; ACA42842
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                                                                                                                                                                                                                                                                                   Claim
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180 240 241 VFCTAIVGAGLGFLWFNTYPAQVFMGDVGSLALGGALGVVAVLVRQEFLLVIMGGVFVVE 300 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME 300 TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR 360 9 GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 61 GPESHFSKRGTPTMGGVMILFAITVSTLLMANLANPAVWFSLFVLLGYGAIGFVDDYRKI 121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 1 MILLILAEYLOOFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND Gaps ; 0 Length 360; 69.4%; Score 1274; DB 6; Length 3 .larity 65.8%; Pred. No. 2.5e-131; Conservative 57; Mismatches 66; Indels Best Local Similarity Matches 237; Conserv Sequence 360 AA; 61 181 241 301 Query Match 셤 ò 8 8 a  $\delta$ 엄 8 셤

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cellular proliferation protein; antibiotic;
                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                Trawick JD,
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                                                E. coli cellular proliferation protein #16.
                                                                                                                                                                                                                                                                                                                        Example 3; SEQ ID NO 10028; 511pp; English.
                                                                                                                                                                                                                                               Ohlsen KL, Zyskind JW,
Xu HH;
AAU34435 standard; protein; 360 AA
                                                                                                                                                           21-MAR-2000; 2000US-0191078P.
26-MAY-2000; 2000US-0206648P.
23-OCT-2000; 2000US-02727P.
27-OCY-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0253625P.
16-FEB-2001; 2001US-0263731P.
                                                                                                                                            21-MAR-2001; 2001WO-US009180
                                                                 Antisense, prokaryotic cel
antibacterial, drug design
                                (first entry)
                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                       WPI; 2001-611495/70.
N-PSDB; AAS52294.
                                                                                        Escherichia coli.
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                                                                                                          WO200170955-A2.
                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto RT,
                                14-FEB-2002
                                                                                                                           27-SEP-2001
               AAU34435;
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Carr GJ;

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, seruginosa and Entercoccus faccalis. The invention is a also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The be used to screen compounds in rational drug discovery programmes. The cantisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent din of the printed specification, but was obtained in electronic format directly from WIPO at the way obtained in electronic format directly from WIPO at the way obtained in electronic format whipo int/pub/published\_pot\_sequences

MLLLAEYLOOPYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND 69.0%; Score 1268; DB 4; Length 360; 66.4%; Pred. No. 1.2e-130; ive 51; Mismatches 70; Indels Query Match
Best Local Similarity 66.4
Matches 239; Conservative

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240 300 241 IVCTAIVGAGLGFLWFNIYPAQVFWGDVGSLALGGALGIIAVLLRQFFLLVIMGGVFVVE 300 301 TLSVMIQVASFKLIGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKIR 360 301 TLSVILQVGSFKIRGQRIFRMAPIHHYELKGWPEPRVIVRFWIISLMLVLIGLATLKVR 360 121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180 1 MLVWLAEHLVKYYSGFNVFSYLTFRAIVSLLTALFISLWMGPRMIAHLQKLSFGQVVRND 61 GPESHFSKRGTPTMGGIMILTAIVISVILWAYPSNPYWCVLVVLVGYGVIGFVDDYRKV 181 YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFABYLLIPNVPGAGELI 241 VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME 셤 ઇ a 걍 g ઠે g 8 8

Bscherichia coli, identification, proliferation, microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition. Escherichia coli protein sequence SEQ ID NO:451. AAG98403 standard; protein; 360 AA (first entry) 21-SEP-2001 AAG98403; AAG98403

RESULT 10

19-DEC-2000; 2000WO-US034419 Escherichia coli WO200148209-A2 05-JUL-2001. 

Zyskind JW; (ELIT-) ELITRA PHARM INC Porsyth RA, Ohlsen KL, WPI; 2001-457376/49. N-PSDB; AAH81459.

99US-0173005P

3-DEC-1999;

Novel nucleic acids encoding proteins required for Escherichia proliferation, useful for screening for antimicrobial agents.

Claim 19; Page 570; 596pp; English.

The present invention describes a purified or isolated nucleic acid sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in genetherapy. Expression of (I) in a microorganism inhibits proliferation of the microorganism, the activity or level of a gene product required for proliferation of the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to therapeutic inhibit bacterial and sequences complementary to sequences required for proliferation can be used as antisense required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences

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that are specific for particular species of microorganisms can be used probes to identify particular microorganism species in clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491 represent cligonuclectides, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                           1 MILILLAEYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND
                                                                                                                                                            YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #14015.
                                                                                                     ; Score 1268; DB 4;
; Pred. No. 1.2e-130;
51; Mismatches 70;
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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N-PSDB; ACA32358.
                                                                                                                  Similarity
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                                                                                  Sequence 360 AA;
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Sequence 360 AA; 181 301 61 301 ABU49996, RESULT 12 ABU49996 ID ABU4 XX AC ABU4 셤 8 g ઠે d à d à Db ઠ 셤 à New antisense nucleic acids, useful for identifying proteins or screening

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The invention relates to an isolated mucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
cucleic acid; (2) a host cell containing the vector; (3) an isolated
cucleic acid; (4) an antibody capable of specifically binding
the polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
cucleic prolypeptide; (5) producing the polypeptide; (6) inhibiting cellular
cucleic proliferation or the activity of agene in an operon required for
proliferation or the activity of a gene in an operon required for
cucleic proliferation, or that inhibits oclinar proliferation; (8)
cucleic proliferation, or that inhibits oclinar proliferation of an
corpulate for proliferation, or that inhibits oclinar proliferation of an
corpulate agene required for cellular proliferation of an
corpulate acts; (9) manufacturing an antibiotic; (10) profiling a
corpulation of an organism and present in a culture or collection of
compound; activity; (11) aculture comprising strains in which the extent
corpulation of an organism. The antisense nucleic acids required
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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121 VRKDTKGLIARWKYFWMSVIALGVAFALYLAGKDTPATQLVVPFFKDVMPQLGLFYILLA
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for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                    Claim 25; SEQ ID NO 56412; 1766pp; English.
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                                             1 MLVWLAEYLVKFYSGFNVFSYLTFRAIVSLLTALFISLWMGPHLIAWLQKLQIGQVVRND
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MILLIABYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND
                                                                                                                        61 GPQSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 TLSVMIQVASFKLJGRRVFRMAPIHHHFBLKGWPDFRVIVRFWIITVILVLIGLATLKKRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU48094 standard; protein; 360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00572851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2003 (first entry)
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Trawick JD,
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N-PSDB; ACA51964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200277183-A2.
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Wall D,
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ABU48094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of the following antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense controlled by the antisense controlled by the antisense controlled by the antisense controlled by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular controlleration or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that inhibits cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway of controlleration, or that inhibits cellular proliferation or the biological pathway in which a proliferation or required for cellular proliferation of the product is a gene on which the test compound that inhibits proliferation of an organism acts; (9) mandfacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or underexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the collection of an organism. The antisense mucleic acids are useful for identifying proteins or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryoric essential genes. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from Wipp are the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen KL,
Forsyth RA,
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                                                                                              Protein encoded by Prokaryotic essential gene #35523.
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65.6%; Pred. No. 2.5e-130;
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 77920; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malone C,
Carr GJ,
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25-0CT-2001; 2001US-0342923P.
06-FEB-2002; 2002US-0362899.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002WO-US009107
                                   (first entry)
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Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELITRA PHARM INC.
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Trawick JD,
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N-PSDB; ACA53866.
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                                                                                                                                                                                                                    fersinia pestis
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                                   19-JUN-2003
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Wang L, Wall D, (ELIT-)

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisonse sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding
                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                              Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen KL,
Forsyth RA,
                                                                        Protein encoded by Prokaryotic essential gene #33621.
                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 25; SEQ ID NO 76018; 1766pp; English.
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Query Match

us-10-089-787-2.rag

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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in equired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required for the product lies or a gene on which the test compound that inhibits proliferation of an compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent confideration of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for required for proliferation in cells changed sureus, S. typhimurium, X. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the provences.
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Sequence 360 AA;

240 GPOSHLSKKGTPTMGGALILTAIAISTLLWADLSNRYVWVVLVVTLLFGAIGWVDDYRKV 120 VPCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQEIVLFIMGGVFVME 300 9 9 1 MLVWLAEHLVKYYSGFNVFSYLTFRAIVSLITALFISLWMGPRMIARLQKLSFGQVVRND IEKNSRGLPSRWKYFWOSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 1 MELLEABYLQQFYKGFGVFQYLTERGILSVETALSESEWLGPWMIRTLQIPQIGQAVRND .; 0 Length 360; 70; Indels 68.8%; Score 1264; DB 6; 66.1%; Pred. No. 3.2e-130; ive 52; Mismatches 70; Query Match Best Local Similarity 66,1<sup>1</sup> Matches 238; Conservative 241 181 241 301 121 301 61 61 g g ò 셤 a ò Db à à à ò

Antisense; prokaryotic essential gene; cell proliferation; drug design. Protein encoded by Prokaryotic essential gene #32789. ABU47262 standard; protein; 360 (first entry) Salmomella typhimurium WO200277183-A2 19-JUN-2003 03-OCT-2002 ABU47262; RESULT 14 

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) an bost cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contiferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway to proliferation or that has an activity against a biological pathway or required for proliferation. Or that inhibits cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product liss pathway in which a proliferation-required gene or its gene product liss or a gene on which the test compound that inhibits proliferation of no organism actes; (9) manufacturing an antibiotic, (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the strains; or (13) identifying the target of a compound that inhibits the creaming proteins or screening for new or collection of compound, a proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for molecules for rational confideration in cells other than S. aureus, S. typhymurium, centured for proliferation in cells other than S. aureus, S. typhymurium, the target prokaryotic essential genes. Note: The sequence data for this control format directly from Willey and processe
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                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                               Zyskind .
Xu HH:
                                                                                                                                                                                                                                 Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                 Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 75186; 1766pp; English
                                                                                                                                                                                                                                    Malone C,
Carr GJ,
                                          21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                       ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                        WPI; 2003-029926/02.
N-PSDB; ACA51132.
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Wall D,
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1 MILLLABYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGPWMIRTLQIPQIGQAVRND Gaps ö Query Match 68.6%; Score 1261; DB 6; Length 360; Best Local Similarity 65.8%; Pred. No. 6.8e-130; Matches 237; Conservative 53; Mismatches 70; Indels ( a

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61 GPESHFSKRGTPIMGGIMILISIVISVLLWAYPSNPYVWCVLVVLIGYGIIGFVDDYRKV 120 121 IEKNSRGLPSRWKYFWQSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180 : |:::|| :||||| || :| || ||:::||
121 VRXDTKGLIARWKYFWMSVIALGVAFALYLVGKDTPATQLVVPFFKDVMPQLGLFYILLS 61 GPQSHLSKKGTPTMGGALILITALAISTLLWADLSNRYVWVVLVVTLLFGALGWVDDYRKV

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YFVIVGSSNAVNLTDGLDGLAIMPTVMVAGALGIFCYLSGNVKFAEYLLIPNVPGAGELI 181 Sequence 360 AA;

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241 IVCTAIVGAGLGFLWFNTYPAQVFMGDVGSLALGGALGIIAVLLRQBFLLVIMGGVFVVF 300
                          VFCAALVGAGLGFLWFNTYPAQVFMGDVGALALGAALGTIAVIVRQBIVLFIMGGVFVME 300
          181
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AAU38482 standard; protein; 360 AA AAU38482;

Salmonella typhi cellular proliferation protein #373. 14-FEB-2002 (first entry)

Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.

Salmonella typhi.

WO200170955-A2

27-SEP-2001

21-MAR-2001; 2001WO-US009180,

completed: May 7, 2004, 08:39:26 le : 63 secs

Search con Job time

21-MAR-2000;

23-WAY-2000; 2000US-02066848P. 26-WAY-2000; 2000US-0207727P. 23-OCT-2000; 2000US-0242578P. 27-NOV-2000; 2000US-0253625P. 22-DEC-2000; 2000US-0257931P. 16-FEB-2001; 2001US-0257931P.

(ELIT-) ELITRA PHARM INC

Carr GJ; Trawick JD, Wall D, Ohlsen KL, Zyskind JW, Xu HH; Haselbeck R, Yamamoto RT,

WPI; 2001-611495/70. N-PSDB; AAS56341.

New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.

Example 3; SEQ ID NO 14075; 511pp; English

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aenraginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins useful feration, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The present sequence is also useful to screen for momologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent clin not form part of the printed specification, but was obtained in electronic format directly from WHO at 

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                                                                                                                                                                                                                                                                                                                                                     61 GPESHFSKRGTPTMGGIMILTAIVISVLLWAYPSNPYVWCVLVVLIGYGIIGFVDDYRKV 120
                                                                                                                                                                                                                                           301 TLSVMIQVASFKLTGRRVFRMAPIHHHFELKGWPDPRVIVRFWIITVILVLIGLATLKLR 360
                                                                                                             120
                                                                                                                                                                    121 IEKNSRGLPSRWKYFWOSVFGIGAAVFLYMTAETPIETTLIVPMLKSVEIQLGIFFVVLT 180
                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                 61 GPOSHLSKKGTPIMGGALILTAIAISTLLWADLSNRXVWVVLVVTLLFGAIGWVDDYRKV
                                                       1 MILLLABYLQQFYKGFGVFQYLTLRGILSVLTALSLSLWLGFWMIRTLQIPQIGQAVRND
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 Length 360;
                            Indels
68.5%; Score 1258; DB 4;
65.8%; Pred. No. 1.5e-129;
iive 52; Mismatches 71;
 Query Match
Best Local Similarity 65.8
Matches 237; Conservative
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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

May 9, 2004, 13:18:04 ; Search time 3219 Seconds (without alignments) 10046.829 Million cell updates/sec	US-10-089-787-1	l atgctcctgctgctggccgaccaccttgaagctgcgttga 1083	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Run on:	Title: Derfect accre.	Sequence:	Scoring table:

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query
No. Score Match Length DB ID
1 629.4 58.1 1293 28 BZ568926 BZ579253 BZ579253 BZ579253 BZ579253 C2 8 56.1 754 28 BZ550302 CC140622 NDL.67G2.

57250 59351 58241 53470	8 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	#6886 11108 33135 33177 42680	ALB28696 ALB28696 AY100671 Zea mays BZ652916 OGANG66TM CD863587 AZO1.107E BQ620395 TALT1164E BJ465499 BJ465499 AL508300 AL508300 CG214539 OGYBX83TH	7.9 AGENY 7.9 AGENY 7.9 ACED 8120 8120 8120 8120 8120 8120 8120 8120	17209 psHB042
9 CC85725 8 BZ55935 9 CC86824 0 AW86347	8 AZ58373 8 AZ57837 8 AZ53574 8 BH15360 4 CF14319	9 CG3111 4 CB6331 4 CB6331 4 CB6498 4 CF1426	AL828696 AY10607 AY10607 BESESSES AD86358 BQ66358 BG46549 AL508300 GG21453	A BO7314 A BO7314 A BO8203 B BO8203 B BO8203 B BO8203 B BO8203 B BO8203 B BO8203 B BO8203 B BO8304 B B B B B B B B B B B B B B B B B B B	4 CF84720
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#### ALIGNMENTS

DNA linear GSS 17-DEC-2002 monas aeruginosa genomic clone uence.	eobacteria, Pseudomonadales;	.E., Sims,E.E., Hastings,M., ng multiple isolates of	USA
BZ568926 pacs2-164_8156.x1 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_8156, genomic survey sequence.	BZ568926.1 GI:27202739 GSS. Pseudomonas aeruginosa Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;	l (Date: L. Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library J. Bacteriol. (2002) In press	Contact: Chris K. Raymond Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, Tel: 206216954 Fax: 206687244 Email: craymond@u.washington.edu Class: shotgun. Location/Qualifiers
RESULT 1 BZ568926 LOCUS DEFINITION	VERSION KEYWORDS SOURCE ORGANISM	AUTHORS TITLE JOURNAL	COMMENT

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ווות הומא
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source

aeruginosa" /organism="Pseudomonas /mol\_type="genomic DNA" /strain="2-164"

ORGANISM

181.1-/0/-200-01-81

REFERENCE AUTHORS

TITLE

/db\_xref="taxon:287" /clone="pacs2-164" /clone=lib="pacs2-164" /note="clinical isolate 2-164 Whole genomic shotgun library."

Gaps ij Length 1293; Ouery Match
58.1%; Score 629.4; DB 28; Length
Best Local Similarity 97.2%; Pred. No. 1.2e-86;
Matches 650; Conservative 0; Mismatches 18; Indels

JOURNAL COMMENT

> 셤 ò g ð d à 원 ò 셤

FEATURES

209 GATCGAGACCACCCTGATCGTGCCGATGCTGAGGGGTCCAGAATCCAGTTGGGCATCTT 150

4

genomic shotgun

1..1253 / organism="Pseudomonas aeruginosa" /mol-type="genomic DNA" /strain="WSH" /db\_xref="taxon:287" /clone="mabl2 6268" /clone="mabl2 6268" /clone=lib="mabl" /note="Environmental isolate. Whole gelibrary."

319 156 379 216 439

276 499 559 396 619 456 619 516 739

GITCAACACCIAICCGGCGCAGGICITCAIGGCCGACGICGGCGCGCIGGCGCI GTTCAACACCTATCCGGCGCGCAGGTCTTCATGGGCGACGTCGGCGCGTTGGCCGCTGGGCGC 509 CGCGCTGGGCACCATCGCGGTGATCGTGCGCCAGGAGATCGTGCTGTTCATCATGGGT-G 883

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GACGCCGCGTCTTCCGTATGCCGCTCCATCCATTTCGAACTGAAAGGCTGGCCGG 1003 GGGTGTTCGTCATGGAAACCCTCTCGGTGATGATCCAGGTCGCTTNCTTCAAGCTGACCG 629 cedectiedecaccardadedatatatadedecedadaaatadatetatatatadadada ses 510 884 570 944

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630 GACGCCGCGTCTTCCGCATGCCGCGATCCATCACCATTTCGAACTGAAAGGCTTGCCGG 689

1064 CCACCTTGA 1072 GCCACTIGA 758

RESULT 2 BZS79253 LOCUS DEFINITION

GSS. Pseudomonas aeruginosa ACCESSION VERSION KEYWORDS SOURCE

BZ579253 bp DNA linear GSS 17-DEC-2002 msh2\_6268.xl msh Pseudomonas aeruginosa genomic clone msh2\_6268, genomic survey sequence.
BZ579253.1 GI:27214314

828

800 ACGICGGCGCGCTGGCGCCCCCCCCCCACCATCGC-GGTGATCGTGCGCCAG Acernoececerroececroececececececacacarcarcecegerarcerececea

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969

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576 799

217 GCCTGCCGAGCCGCTGGAAGTACTTCTGGCAGTCGGTGTTCGGCATCGGCGCCGCCGTGT 277 TCCTCTACATGACTGCCGAAACCCGGATCGAGACCACCCTGATGGTGCGGATGCTGAAGA 320 IGTTCGGTGCCATCGGCTGGGTAGACGACTACCGCAAGGTGATCGAGAAGAAGAACTCCCGTG 560 CGAGCAATGCGGTGAACCTCACCGACGGTCTCGACGGCCTGGCGATCATGCCGACGGTAA 457 recrirecceacacacacarcricracracratereseacaacaraacricaccaacr 740 reacecececercecorregerrerespectacerated acceptance and respect to the second acceptance of t 260 CGCTGCTGTGGGCGGATCTTTCCAACCGCTACGTGTGGGTAGTGCTGGTCGTTACCCTGC 97 cecrecreresecesarentrecaaceeraceratereserasiesreseresereseres 380 GCCTGCCGAGCCGCTGGAAGTACTTCTGGCAGTCGGTGTTCGGCATCGGCGCCCCGTGT 440 TCCTCTACATGACTGCCGAAACCCCGATCGAGACCACCCTGATCGTGCCGATGCTGAAGA 500 GCGTCGAGATCCAGATCTTCTTCGTGGTCCTGACCTACTTCGTCATCGTCGCCT 620 TGGTTGCCGCCCCTGGCCATCTTCTGCTACCTGTCGGGCAACGTGAAGTTCGCCGAGT <u> ACCTGCTGATTCCCAACGTACCGGGCGCCGGCGAGCTGATCGTGTTCTGCGCCGCGCTGG</u> 5; Gaps Length 1253; Query Match 53.6%; Score 580.8; DB 28; Length Best Local Similarity 95.9%; Pred. No. 3.4e-79; Matches 636; Conservative 0; Mismatches 22; Indels 680 ORIGIN ద  $\delta$ g 8 g ð 셤 8 8 ઠે g 8 8 \$ g

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Location/Qualifiers

Location/Qualifiers

Location/Coulding

| organism="Aedes aegypti"
| organism="Aedes aegypti"
| strain="liverpool"
| but xref="taxon:1159" |
| clone="wnb.670:7159" |
| clone="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC140622 SP6 Notre Dame Liverpool Aedes aegypti genomic clone NDL.67G2, genomic survey sequence.
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                                                                                                                                                                                                                                 275
                                                                                                                                                                                                                                                                                                                                                                                                           803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              804 CGGCGCGCTGGCGCTGGGCGCCGCGCTGGGCACCATCGCGGTGATCGTGCCCCAGGAGAT 863
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                                                               334 IGCCGCGCGCTCGCTTCTGCTACCTGTCGGCAACGTGAAGTTCGCCGAGTACCT
                                                                                                                                                                                                                                                                                                                                                       274 GTTGATTCCCTACGTACCGGGCGCCGGCGAGCTGATCGTGTACTGCGCGCACACTGGTCGG
                                                                                                                                                                          TGCCGGCGCTGGGCATCTTCTGCTACCTGTCGGGCAACGTGAAGTTCGCCGAGTACCT
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                                                          CAATGOGGTGAACCTCACCGACGGTCTCGACGGCCTGGCGATCATGCCGACGGTAATGGT
                                                                                               394 CAATGCAGTGAACCTCACCGACGGTCTCGACGGCCTGGCGATCATGCCGACGGTAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             864 CGTGCTGTTCATCATGGGTGGGGTGTTCGTCATGGAAACCCTCTCGGTGATGATCC 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-3543
Fax: 301-838-0549
Email: encactigrory
Library was provided by David Severson
Class: SP6
Class: BAC ends.
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Unpublished (2003)
Contact: Brendan Loftus
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Aedes aegypti
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CC140622.1 GI:30009677
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CC140622
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                                        697 GAANAICGIGCTIGNICATIAIGGGIGGGGGGGGGGGGTCAICGGAAAACCCCTCTICGGI 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
Bacteria; Peruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
(bases 1 to 754)
Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M.,
Burns, J. L., Kaul, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of
Psedomonas e-ruginosa library
J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 TACATGACTGCCGAAACTCCGATCGTCGTCCTAGATCGTGCTGAAGAGAGGTGT
   G-AGATCGTGC-TGTTCATGGGTGGGG--TGTTCGTCATGGAAACCCTCTCGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 CTGTGGGCGGATCTTTCCAACCGCTACGTGTGGGTAGTGCTGGTGGTTACCCTGCTGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGAGCCCCTGGAAGTACTTCTGGCAGTCGGTGTTCGGCATCGGCGCCGCCGTGTTCCTC
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/clone="pacs1-60_2592"
/clone_lib="pacs1-60"
/noce="clinical isolate 1-60 Whole genomic shotgun
library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Center
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 206215954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: craymond@u.washington.edu
Class: shotgun.
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Matches 634; Conserv
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/clone="Notrebame Liverpool-101A24"
/clone lib="Notre Dame Liverpool"
/note="vector: pECBAC1; Site_1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
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BZ559351 GI:27175535
GSS.
Pseudomonas aeruginosa
Pseudomonas aeruginosa
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1026)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
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Matches 454; Conservative 0; Mismatches 171; Indels
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Loftus, B., Shetty, J., Knudson, D. and Severson, D.
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
Unpublished (2003)
Other GSSs: NDL. 101A24. SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
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Tel: 301-838-3543
Fax: 301-838-0208
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/organism="Aedes aegypti"
/mol_type="genomic DNA"
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Library was provided by David
Seg primer: T7
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarthini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.

1 (Dases 1 to 158)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Costa,F.F.,

Rogai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Euch Sci. U.S.A. 97 (7), 3491-3496 (2000)
1. .430
/mol type="genomic DNA"
/mol type="genomic DNA"
/strāin="liverpool"
/db xref="taxon:7159"
/clone="NotreDame Liverpool-44D16"
/clone="NotreDame Liverpool-44D16"
/note="Vector: pBCBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
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Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
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NDL.44D16.SP6 Notre Dame Liverpool Aedes aegypti genomic clone NotreDame Liverpool-44D16, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:287"
/db_xref="pac82-164 1435"
/clone lib="pac82-164"
/note="clinical isolate 2-164 Whole genomic shotgun
Whole-Genome-Sequence variation among multiple isolates of Bededomonas acruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Text: 2066857244
Fext: 2066857244
Fext: 2066857240
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1 (bases 1 to 430)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other GSSS: NDL.44016.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                     aeruginosa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by David Severson
                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                            1. .1026
/organism="Pseudomonas
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Library was provided by Davic
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
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CC868241.1 GI:33228251
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6.6%; Score 72; DB 28; Length 89
Best Local Similarity 44.4%; Pred. No. 0.23;
Matches 291; Conservative 0; Mismatches 365; Indels
Seq primer: M13-Reverse
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 694.
Location/Qualifiers
1. 891
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="FM1:IMSS"."
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//organism="MRNA"
//organism=staxon:9606"
//dev_stage="Adult"
//clone_lib="SN0009"
//orce="Organ: stomach normal; Vector: puc18; Site_l: Smal;
//orce="Organ: stomach normal; Vector: puc18; Site_l: Smal;
//orce="Organ: stomach normal; Vector: puc18; Site_l: Smal;
//orce="Organ: stomach normal; Vector: puc18; Site_l: Smal;
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Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
I (bases 1 to 891)
E Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1: IMSS sheared DNA library
Unpublished (2000)
Contact: Breadan J toftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1: IMSS sheared
DNA library
                                                                                                                                                                                           Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-SN0009-100
A00-206-e02&t3=2000-04-10&td=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence start: 27
High quality sequence story: 158.
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    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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AZ683582.1 GI:11820728
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    332 bp DNA linear GSS 08-DEC-2000 22bl0 Shot-gun genomic library of Rhizobium strain ANU365 Rhizobium AE78334 genomic clone 22bl0, genomic survey sequence. AE578373.1 GI:11605592
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A2535744
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Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 816)
Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: M13; derivative strain of NGR234 cured pNGR234a"
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Laboratoire de Biologie Moleculaire des Plantes Superieures
University of Geneva
1 Chemin de 1/Imperatrice, Chambesy/Geneva 1292, Switzerland
Tel: +44(0)1603450000
Fax: +44(0)1603450045
Email: virginie.viprey@bbsrc.ac.uk
Class: shotgun.
                                                                                                        Rhizobium sp. NGR234
Rhizobium sp. NGR234
Rhizobium sp. NGR234
Rhizobium sp. NGR234
Rhizobium/Agrobacterium group; Rhizobium.
Rhizobium/Agrobacterium group; Rhizobium.
(bases 1 to 332)
Viprsy,V., Rosenthal,A., Broughton,W.J. and Perret,X.
Genetic snapshots of the Rhizobium species NGR234 genome
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Context: Brendan J Loftus
Context: Brendan J Loftus
Context: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3543
Email: bjloftus@tigr.org
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
DNA library
Seq priner: M13-Reverse
Class: shotgun
High quality sequence start: 36
High quality sequence stop: 816.
High quality sequence stop: 816.
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CF143195 529 bp mRNA linear EST 09-SEP-2003
UI-HF-BROD-aqz-b-02-0-UI.rl NIH MGC_S2 Homo sapiens cDNA clone
INAGE:3102243 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 529)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Genome Res. 6 (9), 791-806 (1996)
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/db_xref="fraction: 759"
/db_xref="fraction: 759"
/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Bentamoeba histolytica Site=1: Bst 1; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, LiS. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.; The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoebidae; Entamoeba.

I (bases 1 to 906)
S loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
Unpublished (2001)
Unpublished (2001)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 8343
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shoctun
High quality sequence Start: 15
High quality sequence Start: 15
High quality sequence Stop: 733.
Ince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       906 bp DNA linear GSS 24-SEP-2001
ENTITSBITF Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, genomic survey sequence.
                                                                                                                                                                                                                                                   CONCINCOGIATGGCGCCGATCCATCACCATTTCGAACTGAAAGGCTGGCCGGACCCGCG 1010
                                                                    890
                                                                                                                  647
588 CTTCTTCATCATCATCATCATCATCATCGTCATCTTCATCATCATCATCTTCTTCAT
                                                                                                                                                         Length 906;
                                                                                                                                                                                                                                                                                                                                           CGTGATCGTGCGCTTCTGGATCATCACCGTGATCCTGGTGCTGATC 1056
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No. 1.4;
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Medical Center Dr., Rockville, MD 20850,
                                       Tel: 301 838 0208
Fax: 301 838 9543
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamc
DNA library
Seq primer: M13-Forward
Class: shotgun
Righ quality sequence start: 17
High quality sequence stop: 880.
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                                                                                                                         University of lowa 1375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8265
Fax: 319 335 9565
Email: bento-soares@ulowa.edu
Tissue Procurement: Louis Faudt
Tissue Procurement: Louis Faudt
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/humanfi.html
Seq primer: pXx-5,
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                                                    Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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/db xref="Entanceba histolytica Sheared DNA"
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Entamoeba histolytica HM1: IMSS sheared
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1. .890
/organism="Entamoeba histolytica"
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larity 43.1%; Pred. No. 3.1;
Conservative 0; Mismatches 414;
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OGYBC71TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0640K21,
genomic survey sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoidee, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                1 (bases 1 to 786)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Freser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citck, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                   Gaps
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/mol type="genomic DNA"
/strain="873"
/db ref="taxon:4577"
/clone="ZNMBMa0640K21"
/clone="Lb="XM-7-1.5-KB"
/note="Vector: pBCSK-7, Site 1: HincII; 0.7-1.5-Kb
methylation filtered genomic DNA library"
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Tel: 301-838-5843
Fax: 301-838-0208
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Location/Qualifiers
1. .786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other GSSs: OGYBG71TV
Contact: Cathy Whitelaw
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CG311108.1 GI:34228268
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Other GSSs: OGYBG71TV
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May 9, 2004, 13:30:53 ; Search time 524 Seconds (without alignments) 9362.558 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-10-089-787-1 1083 1 atgctcctgctgctggccga.......ccaccttgaagctgcgttga 1083

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2941586 segs, 2264995651 residues IDENTITY\_NUC Gapoxt 1.0 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Sequence 7913, Ap	Sequence 30469, A	Sequence 31717, A	Sequence 33529, A	Sequence 19657, A	Sequence 7594, Ap	Sequence 23402, A	Sequence 39002, A	Sequence 39834, A	Sequence 9977, Ap	Sequence 258, App	Sequence 5931, Ap	Sequence 20228, A	Segmence 37049. A
Δī	US-09-815-242-7913	US-10-282-122A-30469	US-10-282-122A-31717	US-10-282-122A-33529	US-10-282-122A-19657	US-09-815-242-7594	US-10-282-122A-23402	US-10-282-122A-39002	US-10-282-122A-39834	US-09-815-242-9977	US-09-741-669-258	US-09-815-242-5931	13 US-10-282-122A-20228	IIS-10-282-122A-37049
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### ALIGNMENTS

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APPLICANT: Yamonto, Robert T.
APPLICANT: Yamonto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT PELLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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Patent No. US20020061569A1
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari L.
APPLICANT: Tawick, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Carr, Grant
APPLICANT: Trawick, John
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30469, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Pseudomonas aeruginosa
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-30469
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Best Local Similarity 99.74
Matches 1080; Conservative
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Pred. No. 1.6e-270;
0; Mismatches 3; Indels
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                Query Match
Best Local Similarity 99.7%;
Matches 1080; Conservative
                     FEATURE:

NAME/KEY: CDS

; LOCATION: (1)...(1083)

US-09-815-242-7913
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                                         361 ATCGAGAAGAACTCCCGTGGCCTGCCGAGCCGCTGGAAGTACTTCTGGCAGTCGGTGTTC
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GREAGAL INCOMENTALING

APPLICANT: Wang, Liangeu

APPLICANT: Manot, Carlos

APPLICANT: Maloue, Carlos

APPLICANT: Maloue, Carlos

APPLICANT: Maloue, Carlos

APPLICANT: Maloue, Carlos

APPLICANT: Maloue, Carlos

APPLICANT: Trawick, John

APPLICANT: Trawick, John

APPLICANT: Trawick, John

APPLICANT: Trawick, John

APPLICANT: Trawick, John

APPLICANT: Trawick, John

APPLICANT: Wall, John

APPLICANT: Wall, Male

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILD REPRENCATION NUMBER: US/10/282,122A

CURRENT APPLICANTION NUMBER: G0/290, 30

PRIOR PELING DATE: 2000-00-52

PRIOR PELING DATE: 2000-00-52

PRIOR PELING DATE: 2000-00-52

PRIOR PELING DATE: 2000-00-52

PRIOR PELING DATE: 2000-00-62

PRIOR PELING DATE: 2000-00-62

PRIOR PELING DATE: 2000-00-62

PRIOR PELING DATE: 2000-00-62

PRIOR PELING DATE: 2000-00-63

PRIOR PELING DATE: 2000-00-63

PRIOR PELING DATE: 2000-01-23

PRIOR APPLICATION NUMBER: G0/25,538

PRIOR PELING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: G0/26,636

PRIOR APPLICATION NUMBER: G0/26,636

PRIOR APPLICATION NUMBER: G0/26,636

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PRIOR APPLICATION NUMBER: G0/26,636

PRIOR PELING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: G0/26,636

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PRIOR PRIOR DATE: 2000-10-23

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PRIOR PELING DATE: 2000-00-23

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PRIOR APPLICATION NUMBER: G0/26,636

PRIOR PELING DATE: 2000-00-23

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Best Local Similarity 85.0%;
Matches 917; Conservative ; TYPE: DNA ; ORGANISM: Pseudomonas putida US-10-282-122A-31717 61 181 a

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RESULT 4
US-10-284-122A-33529
Sequence 33529, Application US/10282122A
Sequence 33529, Application US/10282122A
Sequence 33529, Application No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mando, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Vammoto, Robert
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A

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70.8%; Score 767; DB 13; Length 1080;
Best Local Similarity 81.9%; Pred. No. 1.2e-189;
Matches 884; Conservative 0; Mismatches 195; Indels 0
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-05
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PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR PLING DATE: 2001-02-09
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JS-10-282-122A-33529
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.021
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILICATION NUMBER: 60/191,078
PRIOR PILICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-03-26
PRIOR PILING DATE: 2000-03-06
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                    GCGATCATGCCGACGGTGATGGTCGCGGGGGGCGCTGGCCATCTTCTGCTACTTGTGTCGGGG
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                                                           AACGTGAAGTTCGCCGAGTACCTGCTGATTCCCAACGTACCGGGCGCCGGCGCGAGCTGATC
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Sequence 19657, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
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APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
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Pred. No. 7.9e-131;
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PRIOR APPLICATION NUMBERS 1. PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - 8
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 19657
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Sequence 23402, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos
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CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: (0/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELLITRA.011A
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o. US20020061569A1
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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larity 68.6%;
Conservative (
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Best Local Similarity
Matches 743; Conserv
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US-09-815-242-7594
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US-09-815-242-7594
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LENGTH: 1083
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Amelbeck, Robert
APPLICANT: Applicant: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yoreyth, R.
APPLICANT: Xu, H.
TITLE OF INVENION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                 421 GCCTTGGGCGTGCCTTCGCCCTGTATCTGGCGGGGAAGATACCCCCGGGAACGAGCTG 480
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APPLICATION NUMBER: 60/191,078
FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
FILE REPERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR PELING DATE: 2003-02-20
PRIOR PELING DATE: 2003-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-05-24
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/20/335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGGCCCTGGATGATCCGTACCTTGCAGATCCCCCAGATCGGCCAGGCCGTGCGCAACGAC 180
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49.6%; Score 537.6; DB 13; Length
Best Local Similarity 68.6%; Pred. No. 5.4e-130;
Matches 741; Conservative 0; Mismatches 339; Indels
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grancto, Robert
Yamamoto, Robert
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; ORGANISM: Klebsic
US-10-282-122A-23402
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APPLICANT: Xu, H.

TITLE OF INYENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.032.22A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 2000-05-26
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PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/235,625
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                 GCGCAGGTCTTCATGGGCGACGTCGCCGCGCGCGCTGGGCGCCGCGCCGCGCACCATC
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APPLICATION NUMBER: 60/267,636
FILING DATE: 2010-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
Xu, H.
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                                    ACCCTCTCGGTGATGATCCAGGTCGCTTCCAAGCTGACCGGACGCCGCGTCTTCCGT
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47.8%; Score 517.2; DB 9;
Best Local Similarity 67.3%; Pred. No. 1.1e-124;
Matches 729; Conservative 0; Mismatches 354;
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APPLICANT: Syskind, Judith W.
APPLICANT: Trawick, Judith W.
APPLICANT: Trawick, Judith W.
APPLICANT: Trawick, Judith W.
APPLICANT: Trawick, Judith W.
APPLICANT: Tamamaco, Robert T.
APPLICANT: Warmanco, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
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| OTHER INFORMATION: n = A,T,C or G
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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SOFTWARE: Patentin version 3.1
SEQ ID NO 39834
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Pred. No. 5.9e-125;
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Best Local Similarity 67.4%;
Matches 730; Conservative
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sequence 258, Application US/09741669
Patent No. US2002002718A1
GENERAL INFORMATION:
APPLICANT: FORENTH, R. Allyn
APPLICANT: FORENTH, Rari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli FILE REFERENCE: ELITRA.009A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEC ID NOS: 481
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 258
LYPE: DATE
TYPE: DATE
TYPE: DATE
TYPE: DATE
TYPE: ORGANISM: Escherichia coli
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Pred. No. 8.6e-121;
0; Mismatches 363;
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Best Local Similarity 66.5%;
Matches 720; Conservative C
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0; Mismatches 363;
                                                          Query Match
Best Local Similarity 66.5%;
Matches 720; Conservative
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US-09-815-242-5931
i Sequence 5931, Application US/09815242
i Sequence 5931, Application US/09815242
i GENERAL INFORMATION:
i APPLICANT: Haselbock, Robert
APPLICANT: Oblsen, Kari L.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamorco, Robert T.
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APPLICANT: Yamamorco, Robert T.
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APPLICANT: Yamamorco, Robert T.
APPLICANT: Sun H. Howard
ITITE OF INVENTION: Pickryotes
FILE REFERENCE: ELITRA,011A
CURRENT PILLIOTON NUMBER: 60/191,078
PRIOR PILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/263,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/263,939
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/263,308
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; Sequence 37049, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
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Publication No. US20040022122A1
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Publication No. US2004002212A1
APPLICANT: Wang Liangsu
APPLICANT: Walnow, Cherlo
APPLICANT: Malone, Cherlo
APPLICANT: Malone, Cherlo
APPLICANT: Transic, John
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PRIOR PLING DATE: 2000-03-20
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APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H. Forsyth, R.
APPLICANT: Xu, H. Striff, Cation of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 00/31,078
FRIDR APPLICATION NUMBER: 60/206,948
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,948
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     TTCTGGCAGTCGGTGTTCGGCATCGGCGCCGTGTTCCTCTACATGACTGCCGAAACC
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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APPLICANT: Trawick, Johnsel
APPLICANT: Carr, Grant
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Carr, Grant
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: NUMBER: US/10/202,122A
CURRENT ELING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR PLICATION NUMBER: 60/207,727
PRIOR PLICATION NUMBER: 60/242,578
PRIOR PLICATION NUMBER: 60/25,625
PRIOR PLICATION NUMBER: 60/25,931
PRIOR PLICATION NUMBER: 60/25,931
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2001-02-06
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45.3%; Score 490.6; DB 13; Length 1060;
Best Local Similarity 68.2%; Pred. No. 8.9e-118;
Matches 710; Conservative 0; Mismatches 329; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-37049
Mang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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LENGTH: 1060
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Search completed: May
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 480.4; DB 13; Length 1167;
Pred. No. 4e-115;
0; Mismatches 301; Indels 87;
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; TYPE: DNA; ORGANISM: Bordetella pertussis
US-10-282-122A-15193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 778; Conservative
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927 ACCGCCAIAGCCAICAGCACGCTGCTGTGGGCGGATCTTICCAACCGCTACGTGTGGGIA GTGCTGGTCGTTACCCTGCTGTTCGGTGCCATCGGCTGGGTAGACGACTACCGCAAGGTG 

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1-7623   98.7%;   Score 1068.6;   DB 4;   Length 1404;	181 GGTCGCAGTCGCACCTGTCGAAGGGGCACCCGACCAGGGCGCCCCTGTTCTTTCT			
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ATGGAGAAGAACTCCCGTGGCCTGCCGAGCCGCTGGAAGTACTTCTGGCAGTCGTTGTTCTTCTGGCAGTCGTTGTTCTTCTGGCAGTCGTTGTTCTTGTGCAGTGTTTCTGGCAGTCGTTGTTCTTGTGCTGGTTTTCTTGTGCTGGTTTTCTTTTTT	GCGATCATGCCGACGGTAATGGTTGCCGGCGCTGGGGCATCTTCTGCTACCTGTCGGGG  AACGTGAAGTTCGCCGAGTACCTGCTGATTCCCAACGTACCGGGCGCGGCGGAGCTGATC	841 GCGGTGATCGTGCGCCACGAGATCGTGCTGTTCATCATGGGTGCGGTGCTCTTGGAA 900  327 GCGGTGATCGTGGGCCACGAGATCGTGCTGTTCATCATCGGTGCTCTTCGAA 900  327 GCGGTGATCGTGGGCCAGAAATCGTGCTTCTTCATGGTGGGTG		GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield et al. APPLICANT: Marc J. Rubenfield and AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION WHMSER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 7623 LENGTH: 1404 TYPE: DNA TYPE: DNA

OY 1021 CGCTTCTGGATCATCACGTGATCTGGTGCTGATCGGCCACCTTGAAGCTGCT 1080  1342 CGCTTCTGGATCATCACCGTGATCCTGGTGCTGATCGGCCTCGCCCACCTTGAAGCTGCT 1401  OY 1081 TGA 1083  Db 1402 TGA 1083  Db 1402 TGA 1404  RESULT 3  US-09-489-039A-5268  Sequence 5268, Application US/09489039A  Sequence 5268, Application et. al  TITLE OF INVENTION:  APPLICATION:  APPLICATION NUMBER: 1080-01-29  NUMBER OF SEQ ID NOS: 14342  SEQ ID NOS: 14342  SEQ ID NO 5268  TTYPE: DNA  TITLE OF SEQ ID NOS: 14342  SEQ ID NOS: 14342  TYPE: DNA	00   00   00   00   00   00   00   0
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OY 241 ACCGCCATAGCCATCAGCACGCTGCTGTGGGCGAATCTTTCCAACGGCTACGTGGGGTA 300	Query Match 33.8%; Score 366.2; DB 4; Length 1083; Best Local Similarity 58.6%; Pred. No. 7e-74; Matches 635; Conservative 0; Mismatches 448; Indels 0; Gaps 0;
301	Oy 1 AIGCTCCTGCTGCCGAATACCTGCAACAGTTCTACAAGGCCTTCGGCGTCTTCCAG 60
361_ATCGAGAAGAACTCCCGTGGCCGAGCCGCTGGAAGTACTTCTGGCAGTCGGTGTTC  406_GTGCGCAAAGATACCAAAGGCCTGATCGCCCGCTGGAAGTATTTCTGGATGTCGGTGATCCCCGCTGGAAGTATTTCTGGATGTCGGTGATCGCCCGCTGGAAGTATTTCTGGATGTCGGTGATCCCCGCTGAAGTATTTCTGGATGTCGGTGATCCGCTGAAGTATTTCTGGATGTCGGTGATCCGCTGAAGTATTCTGGATGTCGGTGATCCGCTGAAGTATTCTGGATGTCGGTGATCCGCTGAAGTATTCTGGATGTCGGTGATCCGCTGAAGTATTCTGGATGTCGGTGATCCGCTGAAGTATTCTGGATGATCCGCTGAAGTATTCTGGATGTCGAAGTATTCTGGATGTCGAAGTATTCCAGGATCCGCTGAAGTATTCTGGATGTCGAAGTATTCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATCAGAAGTATTCAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGTAGAAGA	61
OY 421 GGCATCGCGCGCGCGCGTCCTCTACATGATGCCCGAAACCCCGATCGAGACCACCTG 480	OY 121 GGGCCTGGATGATGATGATGAGATCCCCCAGATCGGCCGGGCGGG
Qy 481 ATGGGGCGATGCTGAAGAGCGTCGAGATCCAGTTGGGCATCTTCGTGGTCCTGACC 540	Oy 181 GGTCCGCAGTCGCACTGTCGAAGAAGGCCACCCCGACCATGGGCGCGCCCTGATCCTT 240
OY 541 TACTICGICAICGICGGCICGAGCAAIGCGGIGAACCICACGACGGCCTCGGACGCCTG 600  Db 586 TACTICGITAICGIACCGGCAACGCCGICCACGACGACGACGACGACCTGACGACGCCTCGACGGCCTG 645	OY 241 ACCGCCAIAGCCATCAGCAGCTGCTGCTGGGGGGATCTTTCCAACCGCTACGTGGGGTA 300 241 TITTCTATCGCAGTATCAACCTTATTGTGGGGCGCGATTAGATAATTCTTATGTGTGTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGCTCCTGCTGCTGGCCGAATACCTGCAAGAGTTCTACAAGGGCTTCGGCGTCTTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201927 ArgriagicnggCrrgCrgAarArCrrgrrGGrraCgAAACCGCGrrraArGCrafrrCr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCTGACCCTGCGCGCGCATTCTCAGCGTGCTCACCGCGCTGTCGCTGTCGCTGTGGCTG
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Pred. No. 4.6e-72;
0; Mismatches 451;
                                                                                COMPULEA. COMPULEA. COMPULEA. CORRENT ASCII TEXT
SOFTWARE ASCII TEXT
SOFTWARE ASCII TEXT
CURRENT APPLICATION DATA:
FILING DATE: 25-Apr-2000
CLASSIFICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
PRIOR APPLICATION NUMBER: 08/476,102
APPLICATION NUMBER: 08/476,102
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: MACHE MACHE S. MARKE
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELEFAX: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOBLOGY: linear
TOBLOGY: linear
TOBLOGY: linear
                                                           '2 inch diskette
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskett
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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Best Local Similarity 58.4
Matches 632; Conservative
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Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INPORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
TITLE OF INVENTION: The Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
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CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Scier
STREST: 9410 Key West Avenue
CITY: Rockville
STATE: MD
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                                                                                                                                                                                                                                                                                                                                         Score 361.4; DB 4; Length
Pred. No. 4.6e-72;
0; Mismatches 451; Indels
           NAME: KERLEY K. HOOVER
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830I21 base pairs
TYPE: NUCleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                           TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-643-990A-1
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                            33.4%;
                                                                                                                                                                                                                                                                                                                                         33.4 Best Local Similarity 58.4 Matches 632; Conservative
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                                                           GCGATTATGCCTACTGCGCTTGTTGCAGGTGCGTTTGCTTTAATTGCTTGGGCTACAGGT 1202586
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                    GCGATCATGCCGACGGTAATGGTTGCCGGCGCGCTGGGCATCTTCTGCTACCTGTCGGGC 660
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J. Craig Venter
INVENTION: The Nucleotide sequence of
the Haemophilus influenzae
Thereof, and Uses Thereof
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CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
CITY: Rockville,
COUNTRY: USA
ZIP: Z0850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3 1/2 inch diskette COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS V6.22 SOFTWARE: ASCII Tark CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
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Patent No. 6528289
GENERAL INFORMATION:
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Owen White
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US-09-643-990A-1
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NOCLEIC ACID AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAI
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION WINDER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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Pred. No. 5.4e-44;
0; Mismatches 472;
                                                                                           CCTGATCGTGCCGATGCTGAAGAGCGTCGAG
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llarity 52.6%;
Conservative
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US-09-540-236-1218
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US-09-540-236-1218
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Best Local S
Matches 560
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Patent No. 6562948
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC99-03PA
CURRENT FILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2043
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Conservative 0; Mismatches 484
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CHER INFORMATION: Incyte template ID No.;
PUBLICATION INFORMATION:
                                                 Sequence 39, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
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ilarity 52.5%;
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APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
TITE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
TILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SCOTWARE: PERL PROGram
SOCTWARE: PERL PROGram
LENGTH: 100848 TCGAGCAATGCGGTGAACCTCACCGACGGTCTCGACGGCCTGGCCGATCATGCCGACGGTA 112 CTGTGGCCTGGGCCCTGGATGATCCGTACCTTGCAGATCCCCCAGATCGGCCAGGCCGTG -----GAGATCCAGTTGGGCATCTTCGTGGTCCTGACCTACTTCGTCATCGGGC 76689 TTTTCAGCGATTCCATTGGGTTTGGGATTTATTATTGCGACTTATTTTGTGTTTGGCAGGC 619 ATGGTTGCCGGCGCGCTGGGCATCTTCTGCTACCTGTCGGGCAACGTGAAGTTCGCCGAG Gaps Length 100848; 33; Score 232.2; DB 4; Length Pred. No. 3.4e-43; 0; Mismatches 473; Indels 9 ACCACCCTGATCGTGCCGATGCTGAAGAGCGTC-----

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US-09-103-840A-2/c
is Sequence 2, Application US/09103840A
is Sequence 2, Application US/09103840A
is Sequence 2, Application US/09103840A
is GENERAL INFORMATION:
APPLICANT: FLEISCHMAN Robert D.
APPLICANT: FRASER, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITILE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITILE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
ITILE OF INVENTION: DNA SEQUENCES
SOFTWARE PAPILIATION NUMBER: US/09/103,840A
OUTHER TRIANG PAPILIATION VET. 2.1
SEQ ID NOS: 2
IENGTH: 440376S
COTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
CUS-09-103-840A-2
US-09-103-840A-2
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16.2%; Score 175.4; DB 3;
Best Local Similarity 50.9%; Pred. No. 5.3e-30;
Matches 527; Conservative 0; Mismatches 466;
                 TACCTGCTGATTCCCAACGTACCGGGGGGCGCGGCGAA
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                                                                                                                                                                                                                                                                                                Score 175.4; DB 3; Length
Pred. No. 5.3e-30;
0; Mismatches 466; Indels
                                                                                                                                         TYPE: DNA POODACTETIUM tuberculosis ORGANISM: Mycobacterium tuberculosis CTHER INFORMATION: H37Rv US-09-103-840A-1
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.9%;
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          NUMBER OF SEQ ID 1
SOFTWARE: Patentl1
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LENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                      %3-08-311-174-4
; Sequence 4, Application US/08311174
; Patent No. 5556776
; GENERAL INFORMATION:
    APPLICANT: TSUCHIYA, MAKOTO
    APPLICANT: MIWA, KIYOSHI
    TITLE OF INVENTION: BACTERIA
    TITLE OF INVENTION: BACTERIA
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pred. No. 3.7e-21;
0; Mismatches 246;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,174
FILING DATE: 2.5EP-1994
181 ATTGGCCTGGCGACGCTGAAGGTACGTTAA 210
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 046836/1992
FILIND BATE: 04-MAR-1992
ATOMEY/AGENT INFORMATION:
NAME: Oblon, No. 5556776man F.
REGISTRATION NUMBER: 24,618
REPERENCE/DOCKET NUMBER: 10-699-0
TELECOMMUNICATION: INFORMATION:
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TELEFAX: (703) 413-2220
TELER: 24855 OPAT UR
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 54.9%;
Matches 308; Conservative
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Betent No. 6610836

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 2004001
CURRENT RILING DATE: 2000-01-27
PRICE APPLICATION NUMBER: US/09/489, 039A
CURRENT RILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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US-09-489-039A-5281
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LENGTH: 210
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Search completed: May 9, 2004, 15:47:38
Job time : 111 secs
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Sequence 881, Application US/09221017B
Sequence No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSE, Bruce C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON:
STREET: 755 PAGE MILL ROAD
CONTINUE OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF TOWNEY OF 
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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INFORMATION FOR SEQ ID NO: 88
SEQUENCE CHARACTERISTICS:
LENGTH: 2402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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REGISTRATION NUMBER: 33
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US-09-221-017B-881
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Pred. No. 3.8e-17;
0; Mismatches 193;
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                           10.6%;
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Best Local Similarity 54.5
Matches 231; Conservative
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New MraY gene and enzyme of Pseudomonas aeruginosa, useful in vitro assays for screening antibacterial compounds that target cell wall blosynthesis, particularly for screening antibiotics against Pseudomonads.
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P-PSDB; AAB73487.
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AAF86639;
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Aca43847 Prokaryot
Aca41787 Prokaryot
Aca31787 Prokaryot
Aca31787 Prokaryot
Aca53957 Klebsiaryot
Aca51352 Prokaryot
Aca51364 Prokaryot
Aca6340 Salmonell
Aab644 Prokaryot
Aca42179 Prokaryot
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Aca43238 Prokaryot
Aca43179 Prokaryot
Aca23866 Prokaryot
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Maximum Match 100%
Listing first 45 summaries
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/*tag= a
/product= "MraY protein"
/function= "Catalyses the transfer of N-acetylmuramic
acid peptide to a bactoprenol phosphate carrier molecule
in peptidoglycan biosynthesis"
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peptidoglycan biosynthesis; bacterial cell wall; infection;
drug screening; antibacterial; Pseudomonad; G+C rich bacterium;
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ACF65387-0
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
                                                                          ATGGCCCCCATCCATCACCATTTCCAACTGAAAGCCTGGCCGGACCCGCGCGTGATCGTG
                                                                                                              901 ACCCTOTOGGGGATGATCCAGGTCGCTTCGTTCAAGCTGACCGGACGCCGCGTCTTCCGT
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              Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa DNA for cellular proliferation protein #407.
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2000US-020648P.
2000US-020778P.
2000US-025362P.
2000US-025362P.
2000US-025363P.
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Xu HH;
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23-OCT-2000; 2
22-DEC-2000; 2
16-FEB-2001; 2
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Yamamoto RT,
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           encodes a phospho-N-acetylmuramyl-pentapeptide translocase designated Mray. The Mray protein is involved in bacterial cell wall biosynthesis. It catalyses the first step of the membrane cycle of peptidogylycan biosynthesis, i.e., the transfer of an N-acetylmuramic acid peptide to a bactoprenol phosphate carrier molecule. The Mray protein is useful in in vitro assays to screen for antibacterial compounds that target cell wall biosynthesis. Inhibitors of the Mray protein are useful in preventing the growth of Pseudomonas and other G+C rich bacteria. Pseudomonas acruginosa is an opportunistic pathogen which causes infections in patients with burns, neutropenia, or cystic fibrosis. Primers or probes derived from the mray gene are useful in nucleic acid amplification-based assays for detecting the presence of a polynucleotide encoding
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   sequence represents the Pseudomonas aeruginosa mraY gene, which
                                                                                                                                                                                                                                                             Query Match

100.0%; Score 1083; DB 4; Length 1083;
Best Local Similarity 100.0%; Pred. No. 3.5e-209;
Matches 1083; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                 Sequence 1083 BP; 164 A; 350 C; 333 G; 236 T; 0 U; 0 Other;
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362859P.
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  useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The autisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a bloogical pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target proliferation in cells other than S. aureus, S. typhimurium, CC prokaryctic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in cellety swipo.int/pub/published_pot_sequences
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99.6%; Score 1078.2; DB 7; Length 1083;
Best Local Similarity 99.7%; Pred. No. 3.3e-208;
Matches 1080; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                          Sequence 1083 BP; 163 A; 348 C; 336 G; 236 T; 0 U; 0 Other;
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                                                            721 GTGTTCTGCGCCGCGCTGGTCGGCGCCGGCCTCGGCTTCCTCTGGTTCAACACCTATCGG
721 GTGTTCTGCGCCGCGCTGGTCGGCCGCCGCCTCGGCTTCTCTGGTTCAACACCTATCGG
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Xu HH;
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-00522851.
06-MAR-2002, 2002US-0362699P.
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961 ATGGCGCCGATCCATCACCATTTCGAACTGAAAGGCTGGCCGGACCCGCGCGTGATCGTG 1020
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ATCCTGCCGTTCATCAAGGATGTCACCATTCCGTTGGGCGTCGGCTTCGTCGTACTGACC 540
                                                                                            TACTTCGTCATCGTCGGCTCGAGCAATGCGGTGAACCTCACCGACGGTCTCGACGGCCTG
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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Trawick JD,
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P-PSDB; ABU41789.
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                        The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the gene product or that has an activity adminst a blological pathway or required for proliferation, or that has an activity adminst a blological pathway or required for proliferation, or that inhibits cellular proliferation of identifying a gene required for cellular proliferation or the biological corpusion which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound of an organism of the strains is present in a culture or collection of the which each of the strains is present in a culture or collection of the proliferation of an organism. The antisense nucleic acids are undersectived confidential proliferation of an organism. The antisense nucleic acids are useful for an organism or for candidate moleciles for actional and any acceptance or and acids are useful for any and any acceptance or and acids are useful and any acceptance or and acids are useful and any acceptance or and acids are useful and any acceptance or and acids are useful and any acceptance or and acids are useful and any acceptance or and acids are useful and any acceptance or and acids are useful and any acceptance or and acids are useful and any acceptance or and acids and acids and acceptance or acids and acceptance or acids and acceptance o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
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the first antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibitied by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for compliced for proliferation, or that has an activity against a biological pathway or proliferation or that has an activity against a biological pathway or equired for proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits proceed or proliferation of an organism. The antisense nucleic acids required for proliferation in calls other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target of prokaryotic essential genes. Note: The sequence data for this patent did corporated form part of the printed specification, but was obtained in cellectronic format directly from WIPO at the printed potential processed or sequences.
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for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
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Best Local Similarity 81.9%; Pred. No. 1.9e-145;
Matches 884; Conservative 0; Mismatches 195; Indels
                                                                                                                         Claim 14; SEQ ID NO 33529; 1766pp; English
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06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
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Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
Nall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
New PPSDB; ABUZ73917.

New antisense mucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Tor homologous mucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Tor homologous mucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Tor homologous mucleic acid representation of a cell. Also included are: Ct the molecic acid inhibite sproliferation of cell. Also included are: Ct the molecic acid inhibite promoter operably linked to the mucleic acid mucleic acid inhibite promoter operably linked to the mucleic acid mucleic acid inhibite promoter operably linked to the mucleic acid mucleic acid; (3) a host cell consalming the vector; (3) an isolated polypeptide or its fragmant whose expression is inhibited by the antisense mucleic acid; (5) prodicing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operan required for proliferation or that activity of the gene product or that has an activity against a biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acces; (3) manufacturing an antiboric; (10) proliferation of an organism acces; (3) manufacturing an antiboric; (10) proliferation of an organism. The antiboric; (10) proliferation of the strains in which each of the strains is present in a culture compound that inhibits proliferation of an organism. The antiboric; (10) proliferation of an organism acces; (3) determining the except of a compound that inhibits for compound a cultity, (11) a culture comprising strains; or consensing for homologous mucleic acids are useful for which each of the strains is present in a culture organism acces; (3) determining the p
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Score 540.8; DB 7; Length 1080;
Pred. No. 7.9e-100;
0; Mismatches 337; Indels 0;
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Xu HH;
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셤 à 셤 à g ò 쉱 상임 ð 셤 à

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:

of the nucleic acid, inhibite proliferation of a cell. Also included are:

concoling a polypeptide whose expression is inhibited by the antisense nucleic acid, (1) a nost call containing the vector; (1) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding cholypeptide or the fragment whose expression is inhibited by the artisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide of the activity of agene in an operon required for proliferation, (7) identifying a compound that inhibites activity of the gene product or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies car agene on which the test compound that inhibits proliferation of an organism acts, (9) manufacturing an antibiocic, (10) profiling a compound's activity, (11) a culture comprising strains in which the series or underexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 23402; 1766pp; English
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Carr GJ,
08-FBB-2002; 2002US-00072851
06-MAR-2002; 2002US-0362699P
                                                                         (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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P-PSDB; ABU31662.
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Best Local Similarity
Matches 741; Conserv
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Wall
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. 0 49.6%; Score 537.6; DB 7; Length 1080; .larity 68.6%; Pred. No. 3.5e-99; Conservative 0; Mismatches 339; Indels 0; Sequence 1080 BP; 177 A; 302 C; 322 G; 279 T; 0 U; 0 Other;

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Prokaryotic essential gene #32789 BP. ACA51132 standard; DNA; 1083 (first entry) 19-JUN-2003 ACA51132; 

Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene

Salmomella typhimurium.

03-OCT-2002.

480 540 600 600 999 999 720 720 780

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid conding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated considered to the fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular consideration or the activity of a gene in an operon required for proliferation or that has an activity against a biological phemby or required for proliferation, or that inhibits cellular proliferation; (8) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological perhway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocis; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or proliferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational contraction and discovery programs, or for screening homologous nucleic acids are useful for proliferation in cells other than S. aureus, S. typhimurium, contraction formet directly from wire of activities or celled to a proliferation of no secuence of the printed specification, but was obtained in cell control formet directly from wire acquences
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; SEQ ID NO 39002; 1766pp; English.
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Carr GJ,
                                                                                                                                                                                           21-WAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072881.
06-MAR-2002; 2002US-0362699P.
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Best Local Similarity 67.4
Matches 730; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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    Antisense; ds; prokaryotic essential gene; cell proliferation;
drug design; gene.
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Forsyth RA,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 39834; 1766pp; English.
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Carr GJ,
                                                                                                                                                                                                                                                         21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
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                                                                           Salmomella typhi.
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Query Match
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes the messlves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, pseudomonas ascruginosa and Enterococcus faccalis. The invention is also useful for the identification of porential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The proteins can be used to screen compounds in rational drug discovery programmes. The proteins can be used to screen compounds in rational drug discovery programmes. The proteins cold sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed aspecification, but was obtained in 3 Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design. Carr ð Trawick JD, New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids. coli DNA for cellular proliferation protein #16 ď, Wall Claim 27; SEQ ID NO 5931; 511pp; English. ftp.wipo.int/pub/published\_pct\_sequences Zyskind JW, 2000US-0191078P. 2000US-0206848P. 2000US-0207727P. 2000US-0242578P. 2000US-0253625P. 2000US-0257931P. 2001US-0269308P. AASS2294 standard; DNA; 1083 2001WO-US009180 (first entry) Ohlsen KL, Xu HH; (ELIT-) ELITRA PHARM INC. WPI; 2001-611495/70. P-PSDB; AAU34435. Escherichia coli WO200170955-A2. 21-MAR-2000; 2 23-MAY-2000; 2 26-MAY-2000; 2 33-OCT-2000; 2 27-NOV-2000; 2 22-DEC-2000; 2 21-MAR-2001; Haselbeck R, Yamamoto RT, 13-FEB-2002 AAS52294; AASS 2294

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AAH81294, where expression of the mucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibite proliferation of the activity or level of a gene product required for proliferation of the activity or level of a gene product required for proliferation of a microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation con be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as conclained acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical cospeciments AAH81295 to AAH81481 of encode the Escherichia coli proteins coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal coligonal c
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                                                                                                                                                                                                                             Escherichia coli protein encoding nucleotide sequence SEQ ID NO:258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents.
                                                                                                                                                                                                                                                                      antimicrobial; autibacterial; proliferation; microorganism; bacterial growth inhibition; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 386-387; 596pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
AAH81459 standard; DNA; 1083 BP
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Local Similarity 66.5%;
les 720; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-457376/49.
P-PSDB; AAG98403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli,
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                                                                                                                                                        21-SEP-2001
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bose cell containing the vector; (3) an isolated polypeptide; (5) producing the polypeptide; (5) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that that inhibits cellular proliferation; (8) inhibiting cellular proliferation, (9) identifying a gene required for cellular proliferation or the biological pathway required for proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a conspound sactivity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is an entity of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or (13) identifying the target of a compound that inhibits the collection of strains; or cellular proliferation in calls other than S. aureus, S. typhimurium, C. drug discovery programs, or for screening homologous nucleic acids required for proliferation in calls other than S. aureus, S. typhimurium, C. form part of the printed specification, but was obtained in the printed of the printed specification, but was obtained in the parageneral of the printed specification of the printed specification of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                            Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 20228; 1766pp; English
  #14015
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                               21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002; 2002US-0362899P.
06-MAR-2002, 2002US-0362699P.
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    essential
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Trawick JD,
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P-PSDB; ABU28488.
                                                                     drug design; gene.
                                                                                                          Escherichia coli.
                                                                                                                                                  WO200277183-A2
  Prokaryotic
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-)
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Sequence 1083 BP; 190 A; 260 C; 318 G; 315 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences

7; Length 1083;

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                                                                                             ATGCTCCTGCTGCTGCCGAATACCTGCAACAGTTCTACAAGGGCTTCGGCGTCTTCCAG
                                                    Gaps
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Query Match 46.4%; Score 502.2; DB 7; Length Best Local Similarity 66.5%; Pred. No. 4.8e-92; Matches 720; Conservative 0; Mismatches 363; Indels
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Sequence 1060 BP; 180 A; 258 C; 313 G; 309 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibite proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway proliferation or that has an activity against a biological pathway required for proliferation, or that thibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological contains a gene activity; (11) a culture comprising strains or the biological contains acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids are useful for for cellular proliferation in cells other than S. aureus, S. typhimurium, K. pneumonlae or P. aeruginosa. The present sequence data for this patient did core proliferation in cells other than S. aureus, S. typhimurium, content of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
                                                                                                                                                                                          proliferation;
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Forsyth RA,
                                                                                                                                                                                            ds; prokaryotic essential gene; cell
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Yamamoto R,
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                                                                                                                                                           Prokaryotic essential gene #30836.
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342921P.
08-FEB-2002; 2002US-00072851.
06-WAR-2002; 2002US-0362699P.
                                                            ACA49179 standard; DNA; 1060
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Trawick JD,
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P-PSDB; ABU45309.
                                                                                                                                                                                                           drug design; gene
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Wall D,
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GACCCGCGCGTGATCGTGCGCTTCTGGATCATCACGGTGATCCTGGTGCTGATCGGCCTC 1062
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   Length 1060;
Score 490.6; DB 7; Length Pred. No. 1.1e-89; O; Mismatches 329; Indels
   45.3%;
Local Similarity 68.2%;
les 710; Conservative
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description		AY008276 Pseudomon	AE016779 Pseudomon	AE016871 Pseudomon	AE012171 Xanthomon	AE011708 Xanthomon	AE016925 Chromobac	AE008699 Salmonell	AL627265 Salmonell	AE016834 Salmonell	AX189057 Sequence	X51584 Escherichia	AE000118 Escherich	AAISI/ZO SEQUEILCE VEEDS1 10 AD11 2 m	ASSOST E. COLL Z III	TOTAL STREET	AE005185 Escherich	AP002550 Escherich	AE015046 Shigella	AE016978 Shigella	BX640449 Bordetell	BX640434 Bordetell	BX640420 Bordetell	AL646072 Kaisconia	AE0043IU VIDITO CII	AFOUNDESS VIDITIO VI	BASZIOSW NICEOBONIO	AE013965 Yersinia	AJ414143 Yersinia	Vibrio	AP005959 Bradyrhiz	AR388539 Sequence	AC147366 Mus muscu	AE015855 Shewanell	ABOSCOS SNEWAIIETT	BAS/2004 AMOUDSGE	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AE012560 Xylella f	AP002997 Mesorhizo	AL162758 Neisseria	Phot	AX770909 Sequence				DNA linear BCT 19-JUL-2001 Mirr (mirr) Mray (mray), and					eobacteria; Pseudomonadales;		and El-Sherbeini, M.	cluster
ΩΙ	1	AY008276	AE004856 AE016779	AE016871	AE012171	AE011708	AE016925	AE008699	AL627265	AE016834	AX189057	ECMUROY	AE000118			SCOLLOR ADOLESES	AROUT 83	AP002550	AE015046	AE016978	BX640449	BX640434	BX640420	AL646072	AE004310	AP005332	BX321859	AE01975	AJ414143	AP005074	AP005959	AR388539	AC147366	AE015855	AB052554	BX572604	AEO1/218	200000000000000000000000000000000000000	7990004	NMA722491	BX571871	AX770909	ALIGNMENTS			5280 bp		715	4	) B A	Jaa :eria; Gammaproteobacteri	seudomonas.	1 to 5280)	all division gene
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/note="recombinant enzyme catalyzed the ATP-dependent

addition of D-alanine-D-alanine to the

UDP-N-acetylmuramyl-L-alanine-D-glutamate-m-Dap precursor"
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Submitted (02-301-2001) Biochemistry, Merck Research Laboratories,
126 E. Lincoln Avenue, Rahway, NJ 07065, USA
Sequence update by submitter
On Jan 2, 2001 this sequence version replaced gi:10719753.
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6-diaminopimelate ligase"
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               Pseudomonas aeruginosa: cloning, production, and
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TITLE Direct Submission  JOURNAL Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University of Washington, Box 35145, Seattle, WA 98195, USA  Box 35145, Seattle, WA 98195, USA  AUTHORS  JOBSES 1 to 24000)  AUTHORS  JORGEN SELVISSION  TITLE  Submitted (14-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 156, Ganada  COMMENT  This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas acruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by Fions S.L. Britkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.	'Protein name confidence' is used to rate our confidence of the accuracy of the protein name.  Class 1: Function experimentally demonstrated in P. aeruginosa.  Class 2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known).  Class 3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.  Class 4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.		CODS Complement(911308)  // Jocus tag="PA4402" // Jocus tag="PA4402" // Jocus tag="PA4402" // Jocus tag="PA4402" // Jocus studied protein); Subcellular // Jocus to functionally studied protein); Subcellular // Jocus studied protein j. Subcellular // Jocus studied protein name: ornithine // Jocus start=1 // Jo	/db xref="6" (1:995063# ) /translation="MAVGIGPLSTIHPPUGFELGIASAGIKRPGRKDVVVMRCAEGSS" /translation="MAVGIGPLSTIHPPUGFELGIASAGIKRPGRKDVVVMRCAEGSS" /vacvFrinarCaAPVTLAKQRFLGENTXLLITNTGNANAGTGEAGLAAAQTTCAKLAEL AGVAFTYLDTTAKGRAEDEPALAEDEALDALDEADEAAAQTTTDTLERGA SRQFVHDGVTVTVTGISKGGMIKPNMATMLGYIATDAKVAGGVLQDLLEDAANGSFN RITIGGDTSTNDCCMLATGRAALDEVTQASGALFAALGAVLEVGMELAQAIVRDGE GATKVTVVQVNGGATHQECLDVGYAVAHGFLIKTALFASDPNWGRILAAVGRAGVANL DVSKIDVLGDVCIASRGGRAASYTEEQGAAVMAQAEIGIRIELGRGTCSFTIWTTDL SHBYYKINABYRT"  complement (1455 . 4205) /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /gene="seca"   /codon start=1   /transl_table=11   /product="secretion protein Seca"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17241 GGGCCCTGGATGCTACCTTGCAGATCCGCCAGATCGGCCAGGCCGTGCGCAACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GGTCCGCAGTCGCACCTGTCGAAGAAGGCCACCCCGACCATGGGCGGCGCCCTGATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCGCCATAGCCATCAGCACGCTGCTGTGGGCGGGATCTTTCCAACCGCTACGTGTGGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.6%; Score 1078.2; DB 1; Length 24000; llarity 99.7%; Pred. No. 4.7e-131; Conservative 0; Mismatches 3; Indels 0; 0
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39. .712
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complement(1791. .2378)
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9. 712
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 301995)

Selenta, Paulsen; I. Weinel, C., Dodson, R., Hilbert, H., Fouts, D., Gill, S., Paulsen; I. Weinel, C., Madupu, R., Benanan, W., Debby, R., Daugherty, S., Kolonay, J., Madupu, R., Nelson, W., White, O., Peterson, J., Khouri, H., Hance, I., Lee, P., Holtzapple, E., Scanlan, D., Tran, K., Moazzez, A., Utterback, I., Razon, M., Mee, R., X., Koack, D., Tran, K., Moazzez, A., Utterback, I., Holtzapple, E., Scanlan, D., Tran, K., Moazzez, A., Utterback, I., Holtzapple, E., Straetz, M., Heim, S., Kiewitz, C., Eisen, J., Timmis, K., Utesterboft, A., Tummler, B. and Fraser, C.

Complete ganome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440

AL Environ. Microbiol. 4 (12), 799-808 (2002)

SS Nelson, K., Paulsen, I., Weinel, C., Dodson, R., Hilbert, H., Fouts, D., Gill, S., Pop, M., Martins Dos Santos, V., Holmes, M., Brinkac, L., Benan, M., Deboy, R., Daugherty, S., Kolonay, J., Madup, J., Kroack, D., Moestl, D., Wedler, H., Lauber, J., Rizzon, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, J., Rizzon, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, J., Timmis, K., Duesterboft, A., Tummler, B. and Fraser, C.

Submitted (05-NOV-2002) The Institute for Genomic Research, 9712

Medical Conter Dr., Rockville, MD 20850, USA

Location/Qualifiers
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          AACGTGAAGTTCGCCGAGTACCTGCTGATTCCCAACGTACCGGGCGCCCGGCGAGCTGATC
                                                                                                                                           GTGTTCTGCGCCGCCGCTGGTCGGCGCCGGCCTCGGCTTCCTCTGGTTCAACACCTTTCCG
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DAVDPCLCVYPLDEWRGIRALRALPSIREBNRRLQRLIGNAVDLELDGSGRFLVPP
FIRETARLLDRRAMLVGQLNKFQLWDEDAWNAVSAADLAAIQQPGAMPDELRDLIL"
                                                                                                                                                                                                                                                                                                                                                                                AHFQAQQSGQPAPAVQVFDSSRIGSLDDFYRQAQAAGVQLVIGPLEKPLVKQLAAKPQ
LPITTLALNYADAGQKAPPQLFQFGLAAEDEAREVARRARADGMVRAVALVPSGEWGD
RVLAAFRQDWEGNGGTLLAAERIAQPYALAQQTADLPQLRQSEGRARSLQSTVGGSIA
AQPSRQDIPIFLASTPQQAQOIKPTLNFQYAGDVPVYATSNLYSASGDINQYNDWN
GIRFCETPWLLDTSNBLRQQVVQQWPQAGSGLGRLYAMGVDAYSLAFRLGQLKALPDN
RVLGLSGSLSINANQRVERQLPWAEFSGGQVKRLPDTVR"
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GVRKNILYQLALEKGKAE"

GOMPIGHENT (5744. .6164)

/locus tag="Ppl32"

/note="This region contains a gene with one or more
premature stops or frameshifts, and is not the result of a
agequencing artifact, conserved hypothetical protein,
degenerate; similar to GB:X16944, and SP:P15488;
identified by sequence similarity; putative"
                                                                                                                                                                                                                   /product="lipoprotein, putative"
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SDPGYHLVRQARAAGVSVVPVPGACALIAALSAAGLPSDRFIFEGFLPAKQAGRRARL
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PLLGGQAASTNNDAIWALVASLPAEQLQOPTNDQTLAGWTSLAFAVKSAGTLEQQQAA
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6455. .628
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PF02381"
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/note="identified by match to PFAM protein family
PF00590"
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similarity; putative"
                                                                                            / 100us tag="PP1325"

/ 100us tag="PP1325"

/ 100us tag="PP1325"

/ codon_start="P1325"
                                                                               VALOGSHHAGRPLOWLKNAFEC"
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6925. .7872
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4837. .5721
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Pred. No. 8.66-98;
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ilarity 84.9%;
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Best Local Simil
Matches 918; C
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                                              13594 GCCGTCATCGTGCGCCAGGAAATCGTGCTGTTCATCGATGGGCGGCATCTTCGTGGTGGAA 13653
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                                                                                                                                                                                                                                                                                                                                                                                                                     13774 CGTTTCTGGATCATCACCGTGATCTGGTACTGATTGGCCTTGCAACCCTGAAACTGAGG 13833
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Pseudomonas syringae pv. tomato str. DC3000 section 16 of 21 of the
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         GCGCAGGTCTTCATGGGCGACGTCGGCGCGCTGGCGCTGGGCGCCGCGCTGGGCACCATC 840
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                                                                                                              DB 1;
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Pred. No. 6e-91;
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Matches 885,
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I (bases 1 to 13045)

da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R.,

Guaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida
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Camargo,L.E.A., Camarotte,G., Cannavan,F., Cardozo,J.,

Chambergo,F., Ciapina,L.P., Cicarelli,R.M.B., Coutinho,L.L.,

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Jr.R.P., Lemos, B.G.M., Lemos,M.V.F., Locali,E.C., Machado,M.A.,

Madeira,A.M.B.M., Martinez-Rossi,N.M., Martins,E.C., Medanis,J.,

Manck,C.F.M., Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M.,

Okura,V.K., Oliveira,M.C., Oliveira,V.R., Pereira Jr.H.A.,

Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F.,

Takita,M.A., Tamura,R.E., Telxeira,E.C., Tezza,R.I.D., Trindade dos

Santos,M., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and

Kitajima,J.P.

Comparison of the genomes of two Xanthomonas pathogens with

differing host specificities

L. Nature 417 (6887), 459-463 (2002)
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                                                                                                                                                                                                                                                                                         291920 CGTTTCTGGATCATCGCGGATTCTGGTGCTCATCGGCCTTGCCACTGAAACTGAGG 291861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xanthomonas campestris pv. campestris str. ATCC 33913, section 79 of 460 of the complete genome.
AE012171 AE008922
AE012171.1 GI:21113729
                                                                                                                           ATGGCGCCGATCCATCACCATTTCGAACTGAAGCTGGCCGGACCCGCGCGTGATCGTG 1020
                                                                                                                                                                                                                                                   OGCITCTOGATCATCACCTGATCCTGGTGCTGATCGGCCTCGCCACCTTGAAGCTGCGT 1080
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Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade de
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
901 ACCCTCTCGGTGATGCAGGTCGCTTCCTTCAAGCTGACCGGACGCCGCGTCTTCCGT 960
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Xanthomonas campestris pv. campestris str. ATCC 33913
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AUTHORS
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gene

CDS

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7329
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                                                                                                                                                                    6850 ATGCTGCTTGAGCTGGCCCGTTGGCTACAGCAACTGGAGGCCTGTTCGGGCTGTTCAAC
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                                                         Gaps
                                                      ъ,
Length 13045;
Score 598; DB 1; Length 13
Pred. No. 9.9e-69;
0; Mismatches 295; Indels
Query Match
Best Local Similarity 72.6%;
Matches 788; Conservative
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LVSGAIKADDAELHVNPRARSAVIRVAEKLGLGNGESGMGKGNSAAASRFPTADSPFP
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LVDATRPRPATVIVINDPQGKVYYGGLVSAPVFHRVMBGALRLMDVPPDDIGSMLAAQ
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      CDS
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Bacteria, Proteobacteria, Gammaproteobacteria; Xanthomonadales;
Ranthomonadaceae; Xanthomonas.

I (bases 1 to 13079)
Bacteria, Broteobacteria, Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.

I (bases 1 to 13079)
Cashoro, T., Ferro, J.A., Reinach, F.C., Farah, C.S., Furlan, L.R., Quaggio, R.B., Monteiro-Vitcorello, C.B., Van Sluys, M.A., Almeida
Jr., N.F., Alves, L.M.C., do Amaral, A.M., Bertolini, M.C.,
Camargo, L.B.A., Camaroto, F.C., Carantavan, F., Cardozo, J.,
Chamborgo, F., Ciapina, L.P., Formighteri, B.F., Franco, M.C.,
Gramargo, T.C., Ferro, M.I.T., Formighteri, B.F., Franco, M.C.,
Greggio, C.C., Gruber, A., Kateuyama, A.M., Kishi, L.T., Leite
Jr., R.P., Lemos, E.G.M., Lemos, M.V.F., Locali, E.C., Machado, M.A.,
Madeira, A.M. B.N., Martinez-Rossi, N.M., Martins, E.C., Maidanis, J.,
Menck, C.F.M., Miyaki, C.Y., Moon, D.H., Morelia, L.M., Rossi, A., Sena, J.A.D., Silva, C., de Souza, R.F., Spinola, L.A.F.,
Takita, M.A. Tamura, R.E., Teixeira, E.C., Tezza, R. I.D., Trindade dos Santos, M., Truffi, D., Teai, S., White, F.F., Setubal, J.C. and
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S da Silva,A.C.R., Ferro,J.A., Reinach,F.C., Farah,C.S., Furlan,L.R., Quaggio,R.B., Monteiro-Vitorello,C.B., Van Sluys,M.A., Almeida Jr.,N.F., Alves,L.M.C., do Amaral,A.M., Bertclini,M.C., Camargo,L.B.A., Camarotte,G., Cannavan,F., Cardozo,J., Chapina,L.P., Cicarli,F.M.B., Coutinho,L.L., Cursino-Santos,J.R., Bl-Dorry,H., Faria,J.B., Ferreira,A.J.S., Ferreira,R.C.C., Ferro,M.I.T., Formighieri,B.F., Franco,M.C., Greggio,C.C., Gruber,A., Katesuyama,A.M., Kishi,L.T., Leite Jr., K.P., Lecarli,B.C., Machado,M.A., Madeira,A.M.B.N., Martinez-Rossi,N.M., Martins,E.C., Machado,M.A., Mackina,C.F.M., Movo,M.T.M., Okura,V.K., Oliveira,M.C., Oliveira,W.R., Perreira Jr.,H.A., K., Okura,V.K., Oliveira,M.C., Oliveira,V.R., Perreira Jr.,H.A.F., Rossi,A., Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Santos,M., Tamara,R.B., Teixeira,B.C., Tezza,R.I.D., Trindade dos Santos,W., Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and
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Xanthomonas axonopodis pv. citri str. 306, section 86 of 469 of
                                    7870 GIGGGCTTCTGGATCATCTCGGTGCTGGTGCTGATCGGCCTTGCCACGTTGAAGGTG 7929
1018 GIGCGCTTCTGGATCATCACCGTGATCCTGGTGCTGATCGGCCTCGCCACCTTGAAGCTG 1077
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Submitted (28-NOV-2001) Departmento de Bioquimica, Universidade de
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,
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ASGNVYFABYLKIL DIE FGAGELIIICSALAGAGLGFUWRNYFPAMDIGALSLGA
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"codon start=1
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TACCTGACCCTGCGCGCGTTTCTCAGCGTGCTCACCGCGCTGTCGCTGTCGCTGTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7235 GTCAAACGCGATCCCAATGGTTTGAAGTCGCGCTGGAAGTATCTGCTGCAGTCGATCTTC
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prpoaasaippppadgipporailtwrkrrafsvtlpsl"
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ITKILAAKRAARSGAATVIAASREHVILSRLADGEAIGTGVAATTNAVAARKGTWA
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YSSSBARQRIKKSTREIEAALGGYIVEPELIHRDNMVAL"
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3845. .4963

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/BC number="2.7.2.11"

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located using Glimmer/Blastx"
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                                                                                                                                                                                             gene="bioA"
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                                      Chromobacterium violaceum ATCC 12472 section 16 of 16 of the ABO16925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925 AD016925
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The complete genome sequence of Chromobacterium violaceum reveals
remarkable and exploitable bacterial adaptability
Proc. Natl. Acad. Sci. U.S.A. 100 (20), 11660-11665 (2003)
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KELTVGNIWVALGYSNDLFQAQQDAKNAKRPPELAYRPQQEGNVLAIDNMTILKDAPR
PDLAHKFINFMLDGKNASEISNQIGATNPVKAAEAFFKPQIKANPVIMLDPSKGKYVA
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GLWWDALHGFASEPSALSDLDLVYFDAENLSPDREAALQRRLASVHPDLPWEVTNQAA
VHLWFADRFCYPVEPLPSLEAALATWPEYATAVGVALNADDSLRIIAPFGLDDLFAMT
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complement (7321. .8358)
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/locus_tag="CY4214"
complement(6173..6757)
/locus_tag="CY4214"
/noce="identified by sequence similarity; putative;
located using Glimmer/GeneMark/Blastx/COG3575"
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note="identified by sequence similarity, putative,
ccated using GeneMark/Blastx/COG0108"
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Glimmer/GeneMark/Blastx/COG0687/TC:3.A.1.11.2"
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/note="identified by sequence similarity;
located using Blastx"
/codon_atrt=1
/transl_table=11
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protein_id="AAQ61874.1"
db_xref="GI:34105520"
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Pred. No. 2.3e-67;
0; Mismatches 302;
                                                                                                                                                                          substrate-binding protein"
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/db_xref="G1:34105519"
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complement(7321. .8358)
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/gene="ribB"
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Matches 78
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8 8 8 8

TITLE

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="3-isopropylmalate isomerase (dehydratase),
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(SW:LEU2 SALTY)"
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COMDlement (910, 915)
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A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.iggr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The analyses of ribosome binding sites and promoter binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/and Pedro Romero and Peter Karp at EccCyc; http://ecccyc.PangeaSystems.com/ecccyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
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subunit with LeuC"
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(SW:LEUD_SALTY)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413 (6858), 852-856 (2001)
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CONSRTM
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                                                                                                                                                                                  REFERENCE
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17975

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AL627265 251050 bp DNA linear BCT 04-JUL-2003 Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18, complete chromosome; segment 1/20. AL627265 AL513382 AL627265.1 GI:16501283
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Salmonella enterica subsp. enterica serovar Typhi
Bathoria; Proteobacteria; Gammaproteobacteria; Enterobacterials
Enterobacteriaceae; Salmonella.
I (bases I to 2510so)
Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G.,
                                                                                                                                                                                                                                                                                                            18396 GCCGTGCTGCGTCAGGAATTTCTGCTGATCATGGGCGCGCGTCTTTGTGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17616 TATCTGACGTTTCGCCCCATCGTCAGCCTGTTGACCGCGCTGTTCATCTTTTATGGATG 17675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17736 GGCCCGGAATCGCACTTCAGTAACGCGGTACGCCGACGATGGGCGGCATCATGATCCTG 17795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acercantricantricerrendiningederracecerenaaceeracerregies 17855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="putative RBS for leuL; RegulonDB:STMS1H000494"
complement (5271. .5279)
          RegulonDB:STMS1H000492'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for leuO; RegulonDB:STMS1H000495'
                                                                                                                                                   RegulonDB:STMS1H000493
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(SW:LEUU_SALTY)"
                                                                                                                                                                                                                                                                                                                                                                                                                                       (SW:LPL_SALTY)
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                                                                                                                                                                                                                                                                                                                                                                               /gene="leuL"
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47.8%; Score 518.2; DB 1;
Best Local Similarity 67.4%; Pred. No. 2e-58;
Matches 730; Conservative 0; Mismatches 353;
          leuB;
                                                                                                                                                   leuA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative -10 signal
RegulonDB:STMLTH004472"
complement(5290. .5298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="putative -35 signal
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complement(5067. .5153)
                                                                                                                                         /note="putative RBS for
complement (5067. .5298)
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trans1 table=
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gene="leu0"
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Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/S_typhi/). Location/Qualifiers
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/organism="Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CBIO 15A, UK
E-mail: parkhill@sanger.ac.uk
Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Typhi"
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/gene="STY0002"
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3734...5020
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kinases putative ATP-binding proteins, Score 79.20,
E-value 5.7e-21"
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kinase family, score 207.70, E-value 1.7e-58"
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Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Deng,W., Liou,S.-R., Plunkett,G. III, Mayhew,G.F., Rose,D.J.,
Burland,V., Kodoyianni,V., Schwartz,D.C. and Blattner,F.R.
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AE016834.1 GI:29136167
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VERSION
KEYWORDS
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                                                                                                                                                                                                          /note="Orthologue of E. coli yaaA (YAAA_ECOLI); Fasta hit
to YAAA_ECOLI (258 aa), 86% identity in 257 aa overlap"
Codon starr=1
/transI_table=11
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Pred. No. 1.3e-58;
0; Mismatches 353;
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/note="synonym: yaaA"
complement(5114. .5887)
/gene="STY0005"
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Direct Submission
Submitted (25-SBR-2002) Laboratory of Genetics, University of
Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
Location/Qualifiers
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Location/Qualifiers
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/note="unnamed protein product"
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TEABFPLWQHHQDPMAVDKLADGIRKFAVDQEKLEKMIGDLL"
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|note="corresponds to STY0008 from Accession AL513382:
|salmonella typhi CT18"
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VERNNNFASYLHIPYLHAGELVIVOCTAIVOAGLGFLWFNTYPAQVFWGDVGSLALGGA
LGIIAVLLRQEFLLVIMGGVFVVETLSVILQVGSFKLRGQRIFRMAPIHHHYELKGWP
BERTVYFRHISLMLVLIGLATLKVR"
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/note="pot. -35 region"
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IAHLQKLSFGQVVRNDGPESHFSKRGTPTWGGIMILTAIVISVLLWAYPSNPYVWCVL
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1 (Bass 1 to 2608)

Ikeda,M., Wachi,M., Ishino,F. and Matsuhashi,M.

Notleotide sequence involving murb and an open reading frame ORF-Y spacing murF and ffsW in Escherichia coli
Nucleic Acids Res. 18 (4), 1058 (1990)
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Submitted (15-MAR-1990) Flouret B., URA 1131 du Centre National de
Cabulaire, Batimentífique, C N R S, Biochimie Moleculaire et
Sequence independently determined by [3], but authors accept
sequence [1] as definitive.
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Submitted (02-JAN-1989) Ikeda M., Institute of Applied
Microbiology, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku,
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/note="unnamed protein product; ORF-Y (AA 1-360)"
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UDP-N-acetylmuramoyl-L-alanyl-D-glutamate
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|mol_type="genomic DNA"
|db_xref="taxon:562"
|map="2min"
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db xref="G1:42059"

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Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V.
Blattner,F.R., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F.,
Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J.,
Mau,B. and Shao,Y.
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Escherichia coli K12
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequences as determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director)
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                                                                                                                                                                                                                                                                                                                                          1011 ACGCTTTCTGTCATCCTGCAGGTCGGCTCCTTTAAACTGCGCGGACAACGTATTTTCCGC
    AATATGAACTTTGCCAGCTACTTGCATATACCGTATCTGCGACACGCGGGGGAACTGGTT
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Blattner, F.R.
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DKLPEAVERHTGSLNDEWLMAADLIVASPGIALAHPSLSAAADAGIBIVGDIELFCRE
AQAPIVAITGSNGKSTVTTLVGEMAKAAGVNVGVGGNIGLPALMLLDDECELYVLELS
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MPIRGADERCVSFGVNMGDYHLNHQQGETWLRVKGEKVLNVKEMKLSGQHNYTNALAA
LALADAAGLPRASSLKALTTFTGLPHRFEVVLEHNGVRWINDSKATNVGSTEAALNGL
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QAMRLLAPRVQPGDMVLLSPACASLDQFKNFEQRGNEFARLAKELG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCTCCTGCTGCTGCCGAATACCTGCAACAGTTCTACAAGGGCTTCGGCGTCTTCCAG
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                                                                                                        note="unnamed protein product; murD gene product
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                                                                 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 502.2; DB 1;
Pred. No. 3.5e-56;
0; Mismatches 363;
                                                            note="pot, ribosome binding 196. .2512
                                                                                                                                                                     /transl_table=11
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db_xref="G1:42060"

db_xref="G0A:P14900"

db_xref="G0A:P14900"

db_xref="SWISS-PROT:P14900"
                "pot. -10 region"
.1185
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larity 66.5%;
Conservative 0
                       note="
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Best Local Simil
Matches 720; C
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Supported by NIH grants H300301 and H301428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain M31655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with GS Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (GSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotational assignments courtesy of Monica and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gunction="leader; Amino acid biosynthesis: Leucine"
/note="f28; 100 pct identical to LPL_ECOLI SW: P09149"
/codon start=1
/product="lea operon leader peptide"
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/db_xxef="G1.786.23"
/translation="WHYPRIGLILINASSIRGRRVSGIQH"
complement(197. .226)
/note="factor Sigma70; promoter leu; documented +1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="central position to predicted promoter: -319.5"
/bound_moiety="TyrR predicted site"
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'bound_moiety="Lrp predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="central position to predicted promoter: -0.5"
/bound modety="Lexa predicted site"
complement (354, .368)
/note="No predicted promoter"
/bound modety="bry documented site"
complement (354, .368)
/note="central position to leukBCD promoter: -156.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554. .565
/note="central position to predicted promoter:64"
/bound_moiety="AraC predicted site"
646. .1767
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/note="No predicted promoter"
/bound_moiety="LexA predicted site"
complement (201. .221)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Escherichia coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="synonym: b0075"
complement(77. .163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:83333"
complement(77.,163)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/ translation="wemslaanclskigrlmcfthfprqtvrqamemlsgaemvvrsl

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17grypsiskvryadjpipgvlkkaratkgbavvrsbvgqqqqqquspkalatb
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GMVKQWQDMIYSGRHSQSYMOSLPDFVKLABAYGHVGIQISHPHELBSKLSEALEQVR
NNRLVFVDVTVDGSEHVYPMQIRGGGMDEMMLSKTERT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVICHNSOPAVSNAVNALLKVMFNDELFYRYGRGIOFTARAFOLFGSVROALOLVONELP
GSGFEPPASSBRVFHLCVCSPLDSILTSQIYNHIGDTAPNIHYMFKSSLNQNTEHQLRY
GETFFVISVEDFHRPEFTSVDLFKDEMVLVASKNHPTIKGPLLKHDVYNEQHAAVSLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="MTHSTAMDSVFIRTRIFWFSEFYSFCFFLFYMHDKSYSSGLFLC
IPIRERELSVTVELSMPEVQTDHPETAELSKPQLRMYDLNLLTVFDAVMQEQNITRAA
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"Dote="central position to predicted promoter:107.5"

//Dound moiety="Lrp predicted site"

1955...1984

//note="factor Sigma70; promoter ilvIHp2; documented+1 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1802. .1816
/note="central position to predicted promoter: -39.5"
/bound molety="Lrp predicted site"
1813. .1839
/note="factor Sigma70; promoter ilvIHp4; documented+1 at 85394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1833. .1847
/note="central position to predicted promoter: -8.5"
/bound_moiety="Lrp predicted site"
1838. .1866
/note="factor Sigma70; promoter ilvIHp3; documented+1 at
85420"
                                                                                                                                                                                                                                                                                                                                           'product="probable transcriptional activator for leuABCD
                                                        'gene="leu0"
function="putative regulator; Amino acid biosynthesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EC number="4:1.3.18"
function="enzyme; Amino acid biosynthesis: Isoleucine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes="o604; 98 pct identical (1 gap) to 522 residues fromILVI ECOLI SW: P00893 (566 aa)"
/codon start=1
/transl_table=11
/product="acecolactate synthase III, valine sensitive, large subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="central position to predicted promoter:136.5"
bound_moiety="Lrp predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1915. .1929
/note="central position to predicted promoter:73.5"
/bound_moiety="Lxp predicted site"
                                                                                                                                               /note="0373; 100 pct identical to LEUO ECOLI SW:
P10151(290 aa) but contains 59 additional N-ter aa
C-term residues; 100 pct identical to PIR: $40589 k
contains 24 additional C-term residues"
/codon start=1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAC73187.1"
/db_xref="GI:1786264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAC73188.1"
/db_xref="GI:1786265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="synonym: b0077"
note="synonym: b0076"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   978. .1992
note="central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           995. .3809
gene="ilvi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .995. .3809
gene="ilvI"
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gene CDS

/gene="leu0"

13536

15-AUG-2001

13416

13356

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GGTCCTGAATCACACTTCAGCAAGCGCCGGTACGCCGACCATGGGCGGGATTATGATCCTG 12771
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Ayala J.A., Instituto de Biologia Molecular, Centro de Biologia
Universidad Autonoma, Canto-Blanco 28049, Madrid, Spain.
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Ayala J.A.;
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